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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:30:16 1998; MasPar time 4.32 Seconds 278.747 Million cell updates/sec 000

bular output not generated.

>US-08-938-548A-11 (1-33) from US08938548A.pep 256 Description: Perfect Score:

1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 Sequence:

PAM 150 Gap 11 Scoring table:

120441 seqs, 36531193 residues Searched:

Database:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Mean 30.310; Variance 51.743; scale 0.586 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Pred. No.	9.01e-01	1.84e+00	2.63e+00	2.63e+00	3.73e+00	5.28e+00	5.28e+00	7.44e+00	7.44e+00	7.44e+00	1.05e+01	1.05e+01	1.05e+01	1.46e+01	1.46e+01	1.46e+01	1.46e+01	1.46e+01	1.46e+01	1.46e+01	1.46e+01	1.46e+01	1.46e+01
Description	hypothetical protein	dystrophin homolog -	oct2 protein isoform	sperm mitochondrial c	tetracycline-minocycl	Ig alpha chain C regi	Ig alpha chain C regi		gene D3 protein - mou	transcriptional regul	hypothetical protein		beta-fructofuranosida	Omega-aga-ivb (nmr, m	Omega-aga-ivb (nmr, 2	omega-agatoxin-ivb -	omega-agatoxin IVB -	omega-agatoxin III, 8	omega-agatoxin IIIA -	omega-agatoxin III, 8	cell division protein	pigment deposition co	agouti protein precur
ដ	S24303	A41130	860079	A37199	JN0800	AHRB	S09276	S11223	156329	B69764	C64314	I46413	S33920	10MB	10MA	IAGG	A44664	B54252	A42335	A54252	B64052	A46298	137143
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Length DB	147	870	93	143	641	299	338	347	425	479	155	197	589	35	48	48	48	92	92	16	103	131	132
% Query Match	28.1	27.3	27.0	27.0	26.6	26.2	26.2	25.8	25.8	25.8	25.4	25.4	25.4	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0
Score	72	70	69	69	68	67	29	99	99	99	65	65	65	64	64	64	64	64	64	64	64	<b>64</b>	64
Bosult No.	, ,	7	m	4	S	Q	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

hypothetical proteins cysteine proteinses ( hypothetical proteinses ( hypothetical protein  Ig alpha chain C regiannin existent  tetracycline resistant  tetracycline resistant  tetracycline resistant  tetracycline resistant  tetracycline resistant  hypothetical 17.9% pr  laminin-related prote  myosin heavy chain, nonethyl D-aspartate  glutamate receptor, N  N-methyl D-aspartate  SPA2 protein - gast  omega-agatoxin III, 8  gene 34 protein - equ  ureas-associated pro  ured protein - Rlebsi  DNA repair protein RA  myosin heavy chain-B,  myosin heavy chain-B,  myosin heavy chain-B,  ilus #common_name house mouse  revision 13-Jan-1995 #text_cf  fitro and at the time of impla  or  ilus activated during embryonic s  ilus activated during embryonic s  ilus activated during embryonic s  ilus activated during embryonic  sitro and at the time of impla  or  incompanie	cific electric ray nlifornica #common_ evision 03-Aug-199 Dyer, S.M.; Burder 5:1069-1076 nt of the subsyna
93 2 864835 hypoth 94 2 849175 cyptel 50 2 809271 gall 95 2 825479 ampinol 96 2 825479 ampinol 97 2 825479 ampinol 98 2 856479 ampinol 99 2 866633 tetrac 99 2 866633 tetrac 90 2 866633 tetrac 90 2 866633 tetrac 91 2 JH0799 laminol 64 2 847555 laminol 64 2 847555 comega. 66 2 847555 comega. 66 2 84287 nred Bandol 90 2 864859 comega. 60 1 WZBEC7 gene. 90 2 842897 ured Bandol 90 2 864859 comega. 60 1 842807 ured Bandol 90 2 864859 comega. 60 1 842807 ured Bandol 90 2 864859 comega. 61 133110.113. 62 2 842897 ured Bandol 63 2 864859 comega. 64 2 842807 ured Bandol 65 2 84859 comega. 66 1 842807 ured Bandol 67 1 843402 myosin 69 2 864859 comeda. 60 1 843807 ured Bandol 60 1 842807 ured Bandol 60 1 842807 ured Bandol 60 1 842807 ured Bandol 60 1 842807 ured Bandol 60 2 864859 comeda. 60 1 843807 ured Bandol 60 2 864859 comeda. 60 1 843807 ured Bandol 60 2 864859 comeda. 60 1 843807 ured Bandol 60 2 864859 ured Bandol 60 2 864859 ured Bandol 60 2 864859 ured Bandol 60 2 864850 ured Bandol 60 1 864850 ured Bandol 60 2 864850 ured Bandol 60 2 864850 ured Bandol 60 1 864850 ured Bandol 60	Yer Linguist Torpedo ca Yorpedo ca Yorpedo ca Yorpedo ca Yorpedo ca Yorpedo ca Yorpedo ca 110, H.; (1991) 111 a compone 4638
0 369 0 493 6 539 6 6339 6 6339 6 6339 6 6339 6 6339 6 6339 1572 2 1464 2 1464 3 170 8 2007 8 2007 8 2007 8 2007 8 2007 8 2007 8 1169 8 2007 8 2007 8 2007 8 2007 1 1464 1 169 8 1007 8 1169 8 1169 8 1169 8 1169 8 1169 8 1169 8 1169 8 1169 8 1169 8 1160 8 1169 8 1160 8 1169 8 116	dystrophin ho 300k subsynap #formal_name electric ra 03-Aug-1992 # 42130 A41130 A41130 A41130 Dystrophin is ences MUD:9206 A41130 e_type mRNA s
न " थ नंबन्धि ए मध  ० – ० ७	TITLE TITLE ALTERNATE_NAMES ORGANISM DATE ACCESSIONS REFERENCE #authors #journal #title #cross.referen #accesslon #accesslon #accesslon #accesslon #accesslon #accesslon #accesslon #accesslon

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galE
#superfamily Escherichia coli UDPglucose 4-epimerase;
UDPglucose 4-epimerase homology
galactose metabolism; isomerase
                                                                                                                                                           #domain UDPglucose 4-epimerase homology #label 6# #domain 347 #molecular-weight 38225 #checksum 6947
##residues 1-347 ##label ZES
##cross-references EMBL:X53949; NID:g57791; PID:g57792
                                                                             CLASSIFICATION
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#authors
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#title
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SUMMARY
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                                                           *superfamily immunoglobulin C region; immunoglobulin homology duplication; glycoprotein; heterotetramer; immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #Journal Nucleic Acids Res. (1990) 18:5289
#title cDNA from rat cells with reconstitutive galactose-epimerase activity in E. coli.
#cross-references MUID:90384840
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stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger
                                                                                                                                     #domain immunoglobulin homology #label IGG1\
#domain immunoglobulin homology #label IGG2\
#binding_site carbohydrate (Asn) (covalent) #status
predicted
#length 299 #checksum 2361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig alpha chain C region - rabbit (fragment) #formal_name Oryctolagus cuniculus #common_name domestic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UDPGIUCOSE 4-epimerase (EC 5.1.3.2) - rat

UDPGALACTOSE 4-epimerase

#formal_name Rattus norvegicus #common_name Norway rat

18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change

08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
16-Aug-1996
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#length 338 #checksum 2169
                                                                                                                                                                                                                                                          Score 67; DB 1; Length 299;
Pred. No. 5.28e+00;
4; Mismatches 2; Indels
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Pred. No. 5.28e+00;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               #type fragment
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Local Similarity 50.0%;
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Best Local Similarity 50.0%;
Matches 7; Conservative
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2 PLPDCCRQKTC-SC 14
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                                                                                                    plasma
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86-152
189-261
38,286
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Runst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.W.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotlin, A.; Borchert, S.; Borriss, R.; Boursier, L.; Brans,
A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.W.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
Ekrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Fuma, S.; Galiszzi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Golighily, E.J.; Grandi, G.;
Guiseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood,
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A lipopolysaccharide-inducuble macrophage gene (D3) is a member of an interferon-inducible gene cluster and is
                                                          Gaps
                                                                                                                                                                                                                                                                    156329 #type complete
gene D3 protein - mouse
#formal_name Mus sp. #common_name mouse
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
28-Feb-1997
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05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
05-Dec-1997
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#length 425 #molecular-weight 47046 #checksum
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##residues 1-425 #****
Score 66; DB 2; Length 347; Pred. No. 7.44e+00; 4; Mismatches 2; Indels
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Pred. No. 7.44e+00;
10; Mismatches 9; Indels
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##cross-references GB:S62227; NID:g385702; PID:g385703
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  Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 31.0%;
Matches 9; Conservative
                                                                                                            261 CGCRIYNLGTGTG 273
                                                                                                                                                                12 CSCRLYELLHGAG 24
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Fauthors Yu, H.; Rosen, M.K.; Schreiber, S.L.
Fsubmission submitted to the Brookhaven Protein Data Bank, September 1993
Fcross-references PDB:10MB
FGRIT Resolution: not applicable
FROM Determination: NMR
#product beta-fructofuranosidase #status experimental #label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors Yu, H.; Rosen, M.K.; Schreiber, S.L.
#submission submitted to the Brookhaven Protein Data Bank, September 1993
#cross-references PDB:10MA
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Omega-aga-ivb (nmr, 21 structures) - funnel-weaving spider
(Agelenopsis aperta)
                                                                                        #binding_site carbohydrate (Asn) (covalent) #status
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                                                                                                   #disulfide_bonds
#length 35 #molecular-weight 3804 #checksum 7419
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#length 48 #molecular-weight 5281 #checksum 7904
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Omega-aga-ivb (nmr, minimized average struct
funnel-weaving spider (Agelenopsis aperta)
#formal_name Agelenopsis aperta
A51323
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A51322
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#region turn (type I
#disulfide_bonds\
#disulfide_bonds\
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#disulfide_bonds\
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45.5%;
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Best Local Similarity 45.5%;
5; Conservative
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                                                     36,42,170,188,211,
254,259,318,322,
388,463,518,527
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REFERENCE
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Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 19 CCRGRPCRCSM 29

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Qy 6 CCRQRTCSCRL 16

Search completed: Thu Jul 30 09:30:35 1998
Job time: 19 secs.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 09:32:10 1998; MasPar time 1.21 Seconds 159.253 Million cell updates/sec : ao

>US-08-938-548A-11 (1-33) from US08938548A.pep 256 1 QPLPDCCRQKTCSCRLXELLHGAGNHAAGILTL 33 abular output not generated. Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

63816 seqs, 5850866 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5\_COMB 2:PCT9\_COMB 3:backfiles

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 21.451; Variance 82.349; scale 0.260

Statistics:

### SUMMARIES

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	Pred.	.23e+0	.23e+0	23e+0	.23e+0	.23e+0	.23e+0.	29e+01	.29e+0	83e+01	85e+01	85e+01	85e+01	.85e+0	85e+01	.08e+01	.08e+0	556	556	556	24€	24e+02	24€	24€
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22 22 22 22 22 22 22 22 22 22 22 22 22	TT 1 US-08-249- XXXXXX  Sequence 4 Sequence APLIC APPLIC APPLICATION APPLICA
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PRIOR APPLICATION DATA
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ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 40, Application PC/TUS9405083C
GENERAL INFORMATION:
APPLICANT: Robert Sklar, Mark Marchionni,
APPLICANT: David I. Gwynne
TITLE OF INVENTION: METHODS FOR ALTERING
TITLE OF INVENTION: MUSCLE CONDITION
NUMBER OF SEQUENCES: 185
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.K. 91 07566.3
FILING DATE: 10-APRIL-1991
ATGNEEZ AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                        NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/CDOCKET NUMBER: LUD 5250.5
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 638-3884
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 66; DB 2;
Pred. No. 2.23e+0
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SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05083C
FILING DATE: 06-MAY-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,204
FILING DATE: 08-YAR-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059,022
FILING DATE: 06-May-93
ATTORNEY/AGENT INFORMATION:
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SEQUENCE 39 AA; 3760 MW; 6521 CN;
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ilarity 70.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity
Matches 7; Conser
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Sequence 40, Application US/08469569
Patent No. 560632
GENERAL INFORMATION:
APPLICANT: Gooderl, Andrew; Stroobant, Paul;
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
APPLICANT: Chen, Maio Su; Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their
TITLE OF INVENTION: Preparation and Use
NUMBER OF SEQUENCES: 184
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STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTR: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                    Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 AA.
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04585/028W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                    Score 66; DB 2; L
Pred. No. 2.23e+01;
1; Mismatches 1
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OPERATING SYSTEM: PC-DOS
SOFTWATING SYSTEM: PC-DOS
SOFTWATING SYSTEM: PC-DOS
SOFTWATING SYSTEM: PC-DOS
SOFTWATING DATE: 06-UN-1995
CLASSIFICATION NUMBER: US/08/469,569
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION NUMBER: 07/940,389
FILING DATE: 30-UN-1992
PRIOR APPLICATION NUMBER: 07/940,389
FILING DATE: 30-UN-1992
PRIOR APPLICATION NUMBER: 07/97,138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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FILING DATE: 03-APRIL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 40, Application US/08469569
                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
CE 39 AA; 3760 MW; 6521 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: GIL
TITLE OF INVENTION: Pro
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
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Best Local Similarity 70.0%;
Matches 7; Conservative
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Patent No. 5670365
GENERAL INFORMATION:
APPLICANT: Feitelson, Jerald S.
TITLE OF INVENTION: Identification of, and Uses For, Nematicidal
TITLE OF INVENTION: Bacillus thuringlensis Genes, Toxins, and Isolates
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
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Pred. No. 3.29e+01;
3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 STATE: Florida
COUNTRY: USA
REFERENCE/DOCKET NUMBER: MA48DD2.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 amino acids
                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 1167 AA; 131657 MW; 7095219 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/540,104
FILING DATE: 06-0CT-1995
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: SALIWARCHIK, DAVIG
REGISTATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA94.C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,717A
FILING DATE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08620717A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1168 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                  873 PNCCKPAACQC 883
                                                                                                                                                                                                                                                                                                                                                                                          |:||: :| |
4 PDCCRQKTCSC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JT 8
US-08-620-717A-9
                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XXXXX
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                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08026138E
Patent No. 5502166
GENERAL INFORMATION:
APPLICANT: Masayoshi MISHINA
APPLICANT: Masayoshi MISHINA
APPLICANT: MOSEL PROTEINS AND GENES CODING THE SAME
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                            ö
                                                                                    Length 1168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Nishlohata Residence 1-107
STREET: 5214, Nishlohata-machi
CITY: Niigata-shi
STATE: Niigata-ken
COUNTRY: JAPAN
ZIP: 951
COMPUTER READBLE FORM:
COMPUTER READBLE FORM:
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
COMPUTER: MS-DOS v.5
                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 to 1464
CE 1464 AA: 165489 MW: 11224000 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE TYPE: cerebellum
PUBLICATION INFORMATION:
AUTHORS: Masayoshi MISHINA
TITLE: NOVEL PROTEINS AND GENES CODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                       1464 AA
                                                                                 Score 64; DB 1; L. Pred. No. 3.29e+01; 3; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: JP 39563/1992
APPLICATION NUMBER: JP 39563/1992
APPLICATION NUMBER: JP 313155/1992
APPLICATION NUMBER: JP 173155/1992
FILING DATE: 30-JUN-1992
APPLICATION NUMBER: JP 215017/1992
FILING DATE: 12-AUG-1992
APPLICATION NUMBER: JP 303878/1992
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hamburg, C.Bruce
REGISTRATION NUMBER: 22,389
REFERENCE/POCKET NUMBER: F-4551
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MS-DOS v.5
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/026,138E
FILING DATE: 26-FEB-1993
INDIVIDUAL ISOLATE: 167p
SEQUENCE 1168 AA; 131542 MW; 7175894 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFANT: (212) 986-2340
TELEFANT: (212) 986-2340
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1464 amino acids
TYPE: amino acid
STRANDEDNESS: single strand
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08026138E
                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                           Query Match 25.0%;
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: mouse
                                                                                                                                                                                                873 PNCCKPAACQC 883
                                                                                                                                                                                                                                      4 PDCCRQKTCSC 14
                                                                                                                                                                                                                                                                                                                                    RESULT 9

AC XXXXXX

AX XXXXXX

DE SEQUENCE 1, APP11C

XX SEQUENCE 1, APP11C

CC GERERAL INFORMAT

CC COMPUTER: DATE:

CC COMPUTER:

C
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XXXXX

XXXEX8X000000000

RESULT ID US

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APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Santos, Ameurfina D.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS: 53
CORRESPONDENCE ADDRESSE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 61; DB 1; L
Pred. No. 5.85e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24260-104763
                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,800
FILING DATE: 19-OCT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
NAME: Ihnen, Jeffrey L.
NAME: Ihnen, Jeffrey L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 51, Application US/08233788A
Patent No. 5635617
GENERAL INFORMATION:
APPLICANT: Doran, James L.
                                                                                                                       Sequence 23, Application US/08137800 Patent No. 5514774 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 51, Application US/08233788A
                                                                                 Sequence 23, Application US/08137800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NISM: Conus ochroleucus
42 AA; 4618 MW; 9505 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-962-4810
TELEFRA: 202-962-830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 42 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IUPOLGGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 PLP-DCCRQKTCSCRLYEL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
23.8%;
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 PVPSDCCQVSSCW-NLYGL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
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ID US-08-233-788A-51

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AC XXXXXX

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DE

Sequence 51, Applica

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CC Sequence 51, Applic

CC Patent No. 5635617

CC APPLICANT: DOLI
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XXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTE: 20003

COMPUTE: Floppy disk
APPLICATION NUMBER: US/08/477,383
FLING DATE: 19-OCT-1993
PRIOR APPLICATION NUMBER: US 08/084,848
FILING DATE: 19-OCT-1993
PRIOR APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: INDO. Jeffrey L.
REGISTERRENCE/DOCKET NUMBER: 28,957
REGISTERRENCE/DOCKET NUMBER: 24,260-107673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
                                          42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Le
5.85e+01;
                                                                                                                                                                                                                                                                                                                                                                                      Conotoxin Peptides 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 61; D
Pred. No. 5.
                                                                                                                                                                                                         Sequence 23, Application US/08477383
Patent No. 5589340
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Hillyard, David R.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Pepti
                                                                                                                                                                      Sequence 23, Application US/08477383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Conus ochroleucus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PLP-DCCRQKTCSCRLYEL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 23.8%;
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 PVPSDCCQVSSCW-NLYGL 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20005
                   JT 12
US-08-477-383-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Gaps

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5; Indels Length 42;

42 AA

PRT;

STANDARD;

RESULT 13 ID US-08-137-800-23

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MasPar time 7.52 Seconds 67.356 Million cell updates/sec MPsrch\_pp

ular output not generated.

Thu Jul 30 09:29:43 1998;

Run on:

>US-08-938-548A-11 (1-33) from US08938548A.pep Title:

1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

124785 seqs, 15338987 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseg31-2
lipart1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part27 Database:

Mean 22.991; Variance 84.736; scale 0.271 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

									•											
	Pred. No.	6.26e+00	9.46e+00	9.46e+00	3.20e+01	5.80e+01	5.80e+01	7.06e+01	8.59e+01	8.59e+01	8.59e+01	8.59e+01	8.59e+01	8.59e+01	8.59e+01	8.59e+01	8.59e+01	8.59e+01	1.27e+02	1.27e+02
	Description	Porcine complement in	Murine ICE-ced-3 homo	Murine interleukin-1	Lysophosphatidic acid	Xenopus Vq1 protein f	Human uridine diphosp	Sequence of a foot an	Human agout1 signall1	Murine agout1 signall	AG1 toxin.	Calcium channel inhib	A. aperta venom fract	Human agouti signalli	Murine agouti signall	Nematode toxin 167P p	Bacillus thuringiensi	Nematocidal toxin 167	Tarantula spider veno	Human NMDA R2A recept
SUMMARIES	ΙΩ	W12414	R98461	R66767	W29877	P95679	W01619	P20020	W10106	W10105	R45611	R60293	R44209	W10102	W10101	W31504	W10653	W16326	R55088	R55529
	DB	23	18	13	56	Н	20	S	23	23	σ	ᇽ	œ	23	23	27	20	23	ព	10
	% Query Match Length DB	363	373	373	329	102	348	78	45	45	48	48	48	130	131	1167	1167	1168	34	1464
	% Query Match	 30.1	29.3	29.3	27.0	25.8	25.8	25.4	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	24.2	24.2
	Score	 11	75	75	69	99	99	65	64	64	64	64	64	64	64	64	64	64	62	62
	Result No.	 -	7	m	4	'n	9	7	œ	6	10	11	12	13	14	15	16	17	18	19

1.27e+02	1.27e+02	1.27e+02	1.53e + 02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.86e+02	1.86e+02	1.86e+02	1.86e+02	1.86e+02	2.24e+02	2.24e+02	2.24e+02		2.71e+02	2.71e+02	2.71e+02	2.71e+02	2.71e+02	2.71e+02
Human N-methyl-D-aspa Human excitatory amin	Glutamic acid recepto	Rat NMDA receptor sub	A-lineage conotoxin p	Predatory cone snail	Salmonella enteritidi	Human membrane antige	TctA sequence.	Human bg protein asso	Human bg protein asso	Cyn d allergen B1.	Cherry polyphenol oxi	E. coli DNA polymeras	DNA polymerase III ho	APP-HCV-E2 fusion pro	Spider venom peptide	N-terminal sequence o	Funnel-web spider ven	Connexin-32.	Sequence of viper ven	Sequence of viper ven	Ovine FSH beta subuni	Ikaros protein.	Mouse 22B/30B (candid	Murine Lystl long iso
R66039 R80970	R42054	R44192	W12745	W24890	W23579	W27333	R62758	W31950	W31949	R27559	W23671	W36071	R40126	R40115	R05633	R11517	R42948	W37469	P91100	P91095	R10038	R92020	W31948	W23594
173	ω	13	20	23	23	24	12	27	27	'n	56	56	ထ	ထ	1	~	ω	27	m	ო	7	16	27	52
1464	1464	1464	42	42	29	253	374	3672	3801	140	147	334	334	367	33	44	48	283	49	49	129	334	2186	3788
24.2	24.2	24.2	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.4	23.4	23.4	23.4	23.4	23.0	23.0	23.0	23.0	22.7	22.7	22.7	22.7	22.7	22.7
62 62 63	62	62	61	61	61	61	61	61	61	9	9	9	9	9	29	29	59	59	28	28	28	28	28	28
20 21	22		24	25	56	27	78	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

transplant to humans
Claim 3; Page 12-14; 20pp; Japanese.
This protein is a porcine complement inhibitor encoded by pMCPcDNA
(T61098). The DNA is useful for large scale production of
recombinant porcine complement inhibitor, which is useful for
porcine organ transplantation into humans. The DNA clone pMCPcDNA is
also useful in the analysis of the promoter region of porcine complement
inhibitor. DNA encoding porcine complement inhibitor – useful in porcine organ W12414;
24-SEP-1997 (first entry)
Porcine complement inhibitor.
porcine; pig; complement; inhibitor; organ transplantation; 09-JAN-1997. 19-JUN-1996; J01704. 20-JUN-1995; JP-178254. (NIME-) NIPPON MEAT PACKERS INC. (NIHA-) NIPPON HAM KK. (NIHA-) NIPPON HAM KK. WHI: 97-087378/08. W12414 standard; Protein; 363 AA. 363 AA; Sus scrofa. WO9700951-A1. Sequence 

ï Score 77; DB 23; Length 363; Pred. No. 6.26e+00; 7; Mismatches 9; Indels Query Match
Best Local Similarity 39.3%;
Matches 11; Conservative

ä

Gaps

98 plqeacrrkacs-nlpdplngqvsypng 124 1 : | : | : | : | : | : | : | : | 2 PLPDCCRQKTCSCRLYELLHGAGNHAAG 29

셤 ò RESULT

MED AD

RESULT

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WHY: 97-08723/08.

New agouti signal protein peptide(s) and nucleic acids - used for altering melanin prodm., for treating e.g. melasma photo-ageing spots, solar keratosis or vitiligo claim 10; Page 11; 67pp; English.

The sequences given in W10101-29 are biologically active peptides and fragments of the agouti signalling protein (ASP) which have depigmenting activity. These peptides are useful for cosmetic purposes and for clinical application in the prevention or treatment of various hyperpigmentary conditions and diseases such as melasma photoageing spots, solar keratosis, and post-inflammatory hyperpigmentation such as occurs at sites of wound healing. They can also be used to provide enhanced emplanogenesis, for treating eg, vitiligo, leucoderma, some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-5EP-1997 (first entry)

Human agouti signalling protein fragment #2.

Agouti signalling protein; ASP; depigmenting activity; cosmetic;

hyperpigmentary condition; melasma photoageing spots; solar keratosis;
post-inflammatory hyperpigmentation; wound healing; eumelanogenesis;
vitiligo; leucoderma; albinism; hair greying.
                                                                                                                                 DNA corresp. to (part of) foot and mouth disease virus RNA - useful in prepn. of vaccines for producing antibodies against the virus Example; Fig 6; 57pp; English.

The inventors claim a DNA molecule comprising a nucleotide sequence corresp. to all or a portion of foot-and-mouth disease virus RNA (FMDV). The DNA molecule is esp. for a precursor of FMDV capsid protein. It esp. codes for FMDV protein p88 and VPI-VP4. It may code for vp4, VP2, vp3 and VPI contiguously. The inventors also claim a vaccine for stiumlating prodn. of antibodies against FMDV in a mammal which comprises at least one of the above recombinant proteins produced by a host cell transformed with the DNA.
(NATR ) National Res Dev Corp.

(WELL ) Wellcome Foundation Ltd.

Boothroyd JC. Cross GaM, Highfield PE, Winther MD, Rowlands DJ,

Brown F, Harris TJR, Lowe PA;

WPI; 82-26702E/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 64; DB 23; Length 45; Pred. No. 8.59e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 65; DB 5; Length 78; Pred. No. 7.06e+01; 9; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-JAN-1997.
21-JUN-1995; UG-000436.
23-JUN-1995; UG-000436.
(UGSH ) US DEPT HEALTH 6 HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    albinism and hair greying.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 qntcsthtygglhst-thstlvls 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
ID W10105,
AC W10105,
DT 17-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ŕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jr 8
W10106 standard; protein; 45
W10106;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 25.4%;
Best Local Similarity 37.5%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Match 25.0%; Local Similarity 41.2%; Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 papaccdpcascqcrff 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLPDCCRQ-KTCSCRLY 17
                                                                                                                     N-PSDB; N20019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
WO9700892-A2.
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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    anomalies, induction
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                   of local endochondral bone formation in non-union fractures, peridontal applens. requiring bone formation and cartilage repair, eg in the treatment of osteoarthritis.

See also P95679-P95692 and N95097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human mature unidate diphosphate galactose-4-epimerase (UDP-G4E) (W01619) catalyses a reversible reaction between UDP-glucose and UDP-galactose that allows galactose residues to enter into the main pathways of glucose metabolism. A deficiency of the enzyme results in galactosaemia. The amino acid sequence of UDP-G4E was deduced from a cDNA clone (T58301) derived from a human endometrial tumour library. Recombinant UDP-G4E polypeptides can be produced in transformed host (e.g. E. coli, COS, Sf9 insect) cells or expressed in vivo for use in the treatment of UDP-G4E deficiency, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding human uridine diphosphate galactose-4-epimerase – used
                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-APR-1997 (first entry)
Human uridine diphosphate galactose-4-epimerase.
Uridine diphosphate galactose-4-epimerase; UDP-G4E; galactosaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 66; DB 20; Length 340, Pred. No. 5.80e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of a foot and mouth disease virus capsid protein encoded by a region of recombinant plasmid pFA61/t76 Vaccine; antibody; capsid protein; immunogen; antigen;
                                                                                                                                                                  DB 1; Length 102;
5.80e+01;
atches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              galactosaemia
                                                                                                                                                                                                                Mismatches
    congenital craniofacial and other skeletal
                                                                                                                                                                  Score 66;
Pred. No. E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in the treatment and diagnosis of g
Claim 1; Page 43-44; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   W01619 standard; Protein; 348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P20020 standard; Protein; 78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine; antibody; capsid pro
foot and mouth disease.
Foot and mouth disease virus.
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53.8%;
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Best Local Similarity 56.3%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                             34 cpyplyeilngs-nha 48
                                                                                                                                                                                                                                                                                                 12 CSCRLYELLHGAGNHA 27
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22-0CT-1980; GB-034130.
27-NOV-1980; GB-038147.
08-APR-1981; GB-011064.
18-AUG-1981; GB-025150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-NOV-1996.
11-MAY-1995; UO5785.
11-MAY-1995; WO-UO5785.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              24-APR-1997 (first
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lest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J1 H, Rosen CA;
WPI; 96-518666/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 AA;
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                                                                                                                       Sequence
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est Loca Atches 262

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RESULT
11D P2
11D P2
12D P2
12D P2
12D P2
12D P2
13D P2
13D P2
13D P2
14D P2
17D P3
18D P3
18

6; Indels

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Gaps

Matches

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particularly plants for the control of nematodes claims therefore the control of nematodes claims 4; Page 35-39, 44pp; English.

Claim 4; Page 35-39, 44pp; English.

This sequence represents the protein encoded by a polynucleotide of the invention. The polynucleotide of the invention is a sequence from a Bacillus thuringiensis (Bt) isolate selected from PS80/J1, PS158D5, PS167P, PS177F1, PS177G, PS204G4 and PS204G6, that encodes a toxin active against nematodes. This sequence represents the 167P protein, and is a delta-endotoxin protein. The polynucleotides and toxins can be used for the control of nematode pests such as Panagrellus Sequence 1167 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           New agouti signal protein peptide(s) and nucleic acids - used for altering melanin prodn., for treating e.g. melasma photo-ageing pepts, solar keratosis or vitiligo
Claim 5; Page 8-9; 67pp; English.
The sequences given in W10101-29 are biologically active peptides and fragments of the agouti signalling protein (ASP) which have depigmenting activity. These peptides are useful for cosmetic purposes and for clinical application in the prevention or treatment of various hyperpigmentary conditions and diseases such as melasma photoageing spots, solar keratosis, and post-inflammatory hyperpigmentation such as occurs at sites of wound healing. They can also be used to provide enhanced eumelanogenesis for treating eg. vitiligo, leucoderma, some forms of albinism and hair greying.
    Agouti signalling protein; ASP; depigmenting activity; cosmetic; hyperplymentary condition; melasma photcoageing spots; solar Keratosis; post-inflammatory hyperplymentation; wound healing; eumelanogenesis; vitiligo; leucoderma; albinism; hair greying.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nematcode toxin 167P protein.
PCR primer; amplify; nematcode toxic protein; Bacillus thuringiensis; delta-endotoxin gene; nematcode pest control; Panagrellus redivivus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 8.59e+01;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                               /note= "Start of Cysteine-rich motif"
                                                                                                                                                                                                                 "Start of basic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 64; DB 23;
                                                                                                                       1..21
/note= "Signal sequence"
32
                                                                                                                                                                                                                                                                                                                                  21-JUN-1996; U10695.
23-JUN-1995; US-000436.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LT 15
W31504 standard; Protein; 1167
W31504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 41.2%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 papaccdpcascqcrff 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PLPDCCRQ-KTCSCRLY 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MYCO) MYCOGEN CORP.
Fu J, Narva KE, Payne J;
WPI; 97-480163/44.
N-PSDB; T89185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-1997.
21-MAR-1997; U04755.
21-MAR-1996; US-590554.
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Bacillus thuringiensis.
WO9734926-A2.
                                                                                                                                                                                                                    /note-
                                                                                                                                                                                                                                                                                                                                                                                                       Hearing VJ;
WPI; 97-087323/08.
                                                                                                 Mus musculus.
                                                                                                                                                                                                                                                                                       WO9700892-A2
                                                                                                                                                                                                                                                                                                              09-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                               peptide
                                                                                                                                                                                              region
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                                                                                                                            Key
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The sequences given in W10101-29 are biologically active peptides and fragments of the agouti signalling protein (ASP) which have depigmenting activity. These peptides are useful for cosmetic purposes and for clinical application in the prevention or treatment of various hyperpigmentary conditions and diseases such as melasma photoageing spots, solar keratosis, and post-inflammantory hyperpigmentation such as occurs at sites of wound healing. They can also be used to provide enhanced emmelanogenesis for treating eg. vitiligo, leucoderma, some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-1997 (first entry)

Human agouti signalling protein.

Agouti signalling protein; ASP; depigmenting activity; cosmetic;

Agouti signalling protein; ASP; melasma photoageing spots; solar keratosis;

byperpigmentary condition; melasma photoageing spots; solar keratosis;

post-inflammatory hyperpigmentation; wound healing; eumelanogenesis;

vitiligo; leucoderma; albinism; hair greying.
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Example; Page 17; 28pp; English.

The sequence is that of a polypeptide present in fraction K of the venom of Agelenopsis aperta, it blocks calcium channels in cells of both mammals and invertebrates, partic. those affecting neuronal and muscle cells. It may be used in the treatment of angina, hypertension, cardiomyopathles, supraventricular arrhythmia, oesophogeal achalasia, premature labour, and Raynaud's disease. It may also be of use in the study of cell physiology and in the control of invertebrate pests. It may be produced synthetically.
                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                            Score 64; DB 8; Length 48; Pred. No. 8.59e+01; 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 64; DB 23; Length 130
Pred. No. 8.59e+01;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Start of Cysteine-rich motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Start of basic region"
86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note- "Signal sequence"
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           forms of albinism and hair greying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JLT 13
W10102 standard; protein; 130 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .T 14
W10101 standard; protein; 131 AA.
W10101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-SEP-1997 (first entry)
Murine agouti signalling protein.
                                                                                                                                                                                                                                                            25.0%;
larity 45.5%;
Conservative
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Matches 7; Conservative
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23-JUN-1995; US-0004
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                    6 CCROKTCSCRL 16
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WPI; 97-087323/08.
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RESULT ID W1 AC W1 DT 17

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:30:53 1998; MasPar time 3.09 Seconds 267.875 Million cell updates/sec sular output not generated. ou:

>US-08-938-548A-11 (1-33) from USO8938548A.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 Title: Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

69111 seqs, 25083644 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot35 1:swiss1

Mean 31.693; Variance 44.992; scale 0.704 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Posult No.	Score	Query	Length	DB	dī	Description	Pred. No.
1	75	29.3	373	П	ICEB MOUSE	CASPASE-11 PRECURSOR (	5.12e-02
7	73	28.5	260	Н	NMA_HUMAN	PUTATIVE TRANSMEMBRANE	1.20e-01
m	71	27.7	450	~	PPAW_CAEEL	PUTATIVE ACID PHOSPHAT	2.76e-01
4	70	27.3	214	-	R10A_TRYBR	60S RIBOSOMAL PROTEIN	4.17e-01
2	69	27.0	197	Н	MCS MOUSE	SPERM MITOCHONDRIAL CA	6.26e-01
9	69	27.0	461	Н	YULZ_CAEEL	PUTATIVE FORKHEAD-RELA	6.26e-01
7	67	26.2	299	Н	ALC_RABIT	IG ALPHA CHAIN C REGIO	1.40e+00
ω	67	26.2		Н	RE11_SCHPO	MEIOTIC RECOMBINATION	1.40e+00
0	99	25.8	347	Н	GALE_RAT	UDP-GLUCOSE 4-EPIMERAS	2.07e+00
10	99	25.8	348	Н	GALE_HUMAN	UDP-GLUCOSE 4-EPIMERAS	2.07e+00
11	99	25.8	360	Н	PURK_PSEAE	PHOSPHORIBOSYLAMINOIMI	2.07e+00
12	99	25.8	425	Н	IFI5_MOUSE	INTERFERON-ACTIVATABLE	2.07e+00
13	65	25.4	155	Н	Y115_METJA	HYPOTHETICAL PROTEIN M	3.06e+00
14	65	25.4	273	-	MD12_SCHPO	MITOCHONDRIAL INHERITA	3.06e+00
15	64	25.0	16	Н	TXO3_AGEAP	OMEGA-AGATOXIN IIIA.	4.51e+00
16	64	25.0		Н	TX4B_AGEAP	OMEGA-AGATOXIN IVB PRE	4.51e+00
17	64	25.0		Н	BOLA_HAEIN	BOLA PROTEIN HOMOLOG.	4.51e+00
18	64	25.0		Н	AGSW_VULVU	AGOUTI SWITCH PROTEIN	4.51e+00
19	64	25.0	131	Н	AGSW_MOUSE	AGOUTI SWITCH PROTEIN	4.51e+00
20	64	25.0	132	-1	AGSW_HUMAN	AGOUTI SWITCH PROTEIN	4.51e+00
21	64	25.0	493	Н	VPE_VICSA	VACUOLAR PROCESSING EN	4.51e+00
22	63	24.6	236	Н	ECSC_BACSU	PROTEIN ECSC.	6.60e+00
23	63	24.6	477	Н	ANGT_MOUSE	ANGIOTENSINOGEN PRECUR	6.60e+00

DB 1; Length 373;

29.3%; Score 75;

Query Match

6.60e+00	9.61e+00	9.61e+00	9.61e+00	9.61e+00	9.61e+00	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01
TETRACYCLINE RESISTANC	UNC-6 PROTEIN PRECURSO	GLUTAMATE (NMDA) RECEP	GLUTAMATE (NMDA) RECEP	SPA2 PROTEIN.	MYOSIN HEAVY CHAIN, NO	GENE 34 PROTEIN.	UREASE OPERON URED PRO	UREASE OPERON URED PRO	HYPOTHETICAL PROTEIN K	TUBULIN BETA CHAIN.	PRPD PROTEIN.	GLYCINE BETAINE TRANSP	DNA REPAIR PROTEIN RAD	HYPOTHETICAL 37.9 KD P	MITOGEN-ACTIVATED PROT	HYPOTHETICAL 51.7 KD P	TETRACYCLINE RESISTANC	HYPOTHETICAL 118.6 KD	DNA POLYMERASE (EC 2.7	HYPOTHETICAL 133.0 KD	THYROGLOBULIN PRECURSO
TET9_ENTFA	UNC6_CAEEL	NME1_RAT	NME1_MOUSE	SPA2_YEAST	MY SO_HUMAN	VG34_HSVEB	URED_KLEAE	URED_KLEPN	Y129_HUMAN	TBB_TRYBR	PRPD_SALTY	BETP_CORGL	RAD5_YEAST	YHO5_YEAST	NTF6_TOBAC	YMT1_CAEEL	TETM_UREUR	YAF3_SCHPO	DPOL_ADE07	YIC6_YEAST	THYG_BOVIN
Н	Н	~	-1	Н	Н	ч	Н	Н	Н	H	Н	н	Н	н		н	Н	Н	Н	Н	Н
639	612	1464	1464	1466	1976	160	270	270	406	442	483	595	1169	334	371	471	639	1039	1122	1150	2769
24.6	24.2	24.2	24.2	24.2	24.2	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4
63	62	62	62	62	62	61	61	61	61	61	61	61	61	9	9	9	9	9	9	9	9
24	25	. 26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

STANDARD; PRT; 373 AA.	; ET. 35. CREATED.	35,	LAST ANNOTATION UPDA	CURSOR (EC 3.4.22) (ICH-3 PROTEASE).	OR CASPL.		AZOA; CHORDATA; VEKTEBKATA; TETKAPODA; MAMMALIA; NTIA.			X CBA; TISSUE-THYMUS;			YDAN J.;	CHEM. 271:20580-20587(1996).		N.A.			DENABEELE P., DECLERCO W., VAN DEN BRANDE	F., SCHOTTE P., VAN CRI		403:61-69(1997).	ACTIVATION CAS	OSIS EXECUTION (	(AL)	SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14; ALSO KNOWN AS THE	MILY.	G1575318;	н	O	CASPASE_HIS;	CASPASE_CYS; 1.	PROTEASE; AP	79 POTENTIAL.				7		-	
	7. 35.	30,		PRECURSOR (E	CASP11 OR ICH3 OR CASPL.	S (MOUSE).	METAZOA; CHO RODENTIA,			L/6 X CBA; T			H., YUAN J.	EM. 271:2058		OM N.A.	AN;	190206.	N M., VANDEN	MOLEMANS F.		103:61-69(19	N: INVOLVED	IBLE FOR APO	SUBUNIT: HETERODIMER	ITY: BELONGS	FAMILY		н	O		٠.	THIOL PROTEA					206 206		-	
CEB_MOU	P70343; 008735	01-NOV-1997	01-NOV-1997	CASPASE-11	CASP11 OR I	MUS MUSCULUS (MOUSE)	EUTHERIA: R	[1]	SEQUENCE FROM N.A	S		WANG S., MIL	SENBERG	BIOL.	[2]	SEQUENCE FROM N.A.	STRAIN-C3H/AN;	MEDLINE; 97190206	VAN DE CRAEI	VAN LOO G., MOLEMANS	FIERS W.;	FEBS LETT. 4	-!- FUNCTION	RESPONS	-1- SUBUNIT	-!- SIMILAR	CASPASE		EMBL; Y13089;	**		PROSITE; PS(	HYDROLASE; 7	PROPEP	CHAIN	PROPEP	CHAIN	ACT_SITE	ACT SITE	TOT TANCO	
RESULT ID I	S F	ដ	5	Œ	Z C	So	88	RN	RP	2	RX	æ	R.	RL	RN N	RP	ಜ	RX	RA	RA	æ	RL	ខ	ပ္ပ	ខ	ខ	ပ္ပ	DR	DR	DR	DR	DR	ΚM	FT	FJ	FT	FT	FI	FI	Ē	

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Gaps

STITES

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-!- THIS IMMUNOCLOBULIN BELONGS TO THE IGA-G SUBCLASS. IT WAS ISOLATED FROM A RABBIT HOMOZYGOUS FOR A2, N80, DE12,15, F71, G75 HEAVY
  KNIGHT K.L., MARTENS C.L., STOKLOSA C.M., SCHNEIDERMAN R.D.;
NUCLEIC ACIDS RES. 12:1657-1670(1984).
-!- FUNCTION: IG ALPHA IS THE MAJOR IMMUNOGLOBULIN CLASS IN BODY
SECRETIONS. IT MAY SERVE BOTH TO DEFEND AGAINST LOCAL INFECTION
AND TO PREVENT ACCESS OF FOREIGN ANTIGENS TO THE GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZESCHNIGK M., WILCKEN-BERGMANN B., STARZINSKI-POWITZ A.;
NUCLEIC ACIDS RES. 18:5289-5289(1990).
-!- FUNCTION: CATALYZES TWO DISTINCT BUT ANALOGOUS REACTIONS: THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RATIUS NORVEGICUS (RAI).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
UDP-GLUCOSE 4-EPPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACCOSE 4-EPPIMERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 67; DB 1; Length 923;
Pred. No. 1.40e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 67; DB 1; Le
Pred. No. 1.40e+00;
4; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               923 AA; 107418 MW; B51C7725 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                          594CED7C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST SANNOTATION UPDATE)
MEIOTIC RECOMBINATION PROTEIN REC11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 97231330.
LI Y.F., NUMATA M., WAHLS W.P., SMITH G.R.;
MOL. MICROBIOL. 23:869-878(1997).
EMBL; U70737; G1619901; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  923 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 CCDIMRCLCLIVNKLSEKSNQTAEILVL 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 CCRQKTCSCRLYELLHGAGNHAAGILTL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                          299 AA; 32256 MW;
                                                                                                                                                                                                                                                                                                 HSSP; P01857; 1PFC.
PROSITE; PS00290; IG_MHC; 2.
IMMUNOGLOBULIN C REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match
Local Similarity 35.7%;
hes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.2%;
Similarity 50.0%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                       CHAIN HAPLOTYPE.
EMBL; X00353; G1576; -.
PIR; A02174; AHRB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-SKELETAL MUSCLE;
MEDLINE; 90384840.
                                                                                                                                       IMMUNOLOGIC SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PLPDCCRQKTC-SC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 PFPDCCPANSCCTC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 8
RE11_SCHPO
Q92380;
                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CT 9
GALE_RAT
P18645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEIOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULTANDE SERVICA SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
           STABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
STRUCTURE OF THE SPERM MITOCHONDRIA.

-1 - SUBCELLUIAR LOCATION: KERATINOUS MITOCHONDRIAL CAPSULE.

-1 - TISSUE SPECIFICITY: TESTIS.

-1 - DEVELOPMENTAL STAGE: LATE MEIOTIC AND EARLY HAPLOID CELLS.

EMBL; M88463; G457886; -:

EMBL; M89463; G567228; -.

PIRS: A37199; A37199.

HSSP; P01058; 11AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORYCTOLAGUS CUNICULUS (RABBII).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 69; DB 1; Length 461;
Pred. No. 6.26e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                               MITOCHONDRION; SELENIUM; SPERM; TESTIS; SPERMATOGENESIS.
BINDING 7 7 SELENIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
101-NOV-1997 (REL. 35, LAST ANNORATION UPDATE)
PUTATIVE FORKHEAD-RELATED TRANSCRIPTION FACTOR F26A1.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WORMPER; F26A1.2; CE02683.
PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK_HEAD_2; 1.
HYPOTHETICAL PROTEIN; DNA-BINDING; NUCLEAR PROTEIN;
HYPOTHETICAL PROTEIN; DNA-BINDING; NUCLEAR PROTEIN;
DNA_BIND 171.
ENGREPHOR REGULATION.
FORK-HEAD.
SEQUENCE 461 AA; 54171 MW; FB2C37B7 CRC32;
                                                                                                                                                                                                                                                                        SELENIUM.
SELENIUM.
SELENIUM.
W; 4E56990C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 69; DB 1; Losted. No. 6.26e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-1- SIMILARITY: CONTAINS A FORK-HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
03 ALPHA CHAIN C REGION (FRAGMENT).
0RYCTOLAGUS CUNICULUS (RABBIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                               34 34 S
197 AA; 21015 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   . Similarity 71.4%;
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 27.0%;
Best Local Similarity 35.3%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221 RHVLCKCQLFDVLQVEG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: | |:|:::|: |
8 ROKTCSCRLYELLHGAG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 PLKPPCCPQK-CSC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PL-PDCCRQKTCSC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U27312; G860690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUTHERIA; LAGOMORPHA.
                                                                                                                                                                                                                 MGD; MGI:96945; MCS
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BRISTOL N2;
FULTON L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
MEDLINE; 84144059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 6
YUL2_CAEEL
Q19802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALC_RABIT
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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RESULT

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Gaps

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RESULT

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BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLATTON R.A., GCCANE J.D.,
KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,
OVERBEER R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
OTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.M., HANNA M.C.,
COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORDOVSKY M.,
KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
EMBL. 167469; G1498882; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                               METHANOCOCCUS JANNASCHII.
ARCHAEBACTERIA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 65; DB 1; Length 273;
Pred. No. 3.06e+00;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BERGER K.H., SOGO L.F., YAFFE M.P.;
SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-- SIMILARITY: TO YEAST MDM12.
EMBL; UG4674; G1655884; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 65; DB 1; L
Pred. No. 3.06e+00;
2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 AA; 17727 MW; 9D9D61E8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 AA; 30517 MW; 9024B3CC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                         01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROTEIN MJ0115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1993 (REL. 27, CREATED)
01-0CT-1993 (REL. 27, LAST SEQUENCE UPDATE)
01-FED-1994 (REL. 28, LAST ANNOTATION UPDATE)
0MEGA-AGATOXIN IIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 AA.
                                         155 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRIAL INHERITANCE COMPONENT MDM12.
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ilarity 53.8%;
Conservative
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ilarity 53.3%;
Conservative
                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 CCKITKPCPYRDYEL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 CCR-QKTCSCRLYEL 19
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
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Q92377;
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P33034;
                                         Y115_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
RESULT 110 Y11 PO 110 Y11 PO 110 PO 100 PO 1
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:31:28 1998; MasPar time 5.40 Seconds 257.359 Million cell updates/sec ü

>US-08-938-548A-11 (1-33) from USO8938548A.pep 256 ular output not generated

Description: Perfect Score:

1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 Sequence:

PAM 150 Gap 11 Scoring table:

140542 seqs, 42109429 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl5
1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Mean 30.295; Variance 46.908; scale 0.646

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ø			SUMMARIES		
Result		Query					
No	Score	Match	Match Length	82	A	Description	Pred. No.
г	77	30.1	363	4	002839	PORCINE MEMBRANE COFAC	5.22e-02
7	74	28.9	750	ო	093473	F14B4.1 (FRAGMENT).	1.77e-01
m	73	28.5	683	က	022187	T05A1.3.	2.65e-01
4	73	28.5	1876	m	024453	PHOSPHOINOSITIDE 3-KIN	2.65e-01
'n	73	28.2	1876	m	001938	PHOSPHOINOSITIDE 3-KIN	2.65e-01
9	73	28.5	1876	m	024209	PHOSPHOINOSITIDE 3-KIN	2.65e-01
7	72	28.1	147	10	261639	3' ORF.	3.94e-01
80	72	28.1	815	σ	033367	DNA GYRASE B SUBUNIT.	3.94e-01
6	70	27.3	426	m	001969	SIMILAR TO GALACTOKINA	8.65e-01
10	70	27.3	883	12	091493	DYSTROPHIN (FRAGMENT).	8.65e-01
11	89	26.6	641	σ	048791	TET.	1.87e+00
12	89	26.6	646	σ	048712	TETRACYCLINE RESISTANC	1.87e+00
13	89	26.6	1382	12	090975	TYROSINE KINASE.	1.87e+00
14	99	25.8	479	σ	P94426	HOMOLOGUE OF REGULATOR	3.99e+00
15	65	25.4	197	4	028584	KAP5.5 KERATIN PROTEIN	5.80e+00
16	65	25.4	589	Н	013388	BETA-D-FRUCTOFURANOSID	5.80e+00
17	64	25.0	310	m	001473	COSMID CO4E6.	8.38e+00
18	64	25.0	369	σ	P75863	FROM BASES 996879 TO 1	8.38e+00
19	64	25.0	397	σ	044258	1-CARBOXY-3-CHLORO-3,4	8.38e+00
20	64	25.0	398	ო	018373	SELD PROTEIN.	8.38e+00

8.38e+00 1.21e+01 1.21e+01 1.21e+01	1.21e+01 1.21e+01 1.21e+01	1.21e+01 1.21e+01 1.21e+01	1.21e+01 1.21e+01	1.21e+01 1.73e+01	1.73e+01 1.73e+01	1.73e+01 1.73e+01	1.73e+01 1.73e+01	1.73e+01 1.73e+01	1.73e+01	2.47e+01 2.47e+01
SELENOPHOSPHATE SYNTHE REPRESSOR/INDUCER PROT COSMID C27A2.	T21B10.6. F21C3.1. AMINO ACID TRANSPORTER	TETRACYCLINE RESISTANC TETRACYLINE RESISTANCE ORF11.		TO EGF MYOSIN	ໝູ	MAJ, COM	NONMUSCLE MYOSIN HEAVY T24D5.1.	N-METHYL-D-ASPARTATE R N-METHYL-D-ASPARTATE R		TRKB (FRAGMENT). MYOSIN HEAVY CHAIN, NO
018597 005606 018238 004393	Q22627 Q19671 Q39135	Q53770 Q67709 Q57224	Q47810 Q17336	Q18857 Q27991	Q12989 Q27990	033700 Q62707	Q62706 Q22732	Q12879 Q63728	008948	Q91373 Q02015
ოთოთ	m m œ	9119	თ ო	m 4	04	10	30	707	10	12
398 146 188 227	366 405 466	639 639 639	639	2946 99	109	157 272	282 304	1464	1464	282 2007
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2222	222	7 7 7	24	2 2	7 7 7	7 7	2 2	2 4	24	333
63 63 63	63 63 63	63 63 63	63 63	63 62	62	62 6	62 62 63	62 62	62	61 61
23 23 24 24	25 26 27	30 30 30 30	31 32	ю 6 4	36.35	37 38	39 40	<b>4</b> 4	43	4 4 5 0

### ALIGNMENTS

Gaps [1]
MEDLINE: 97343414.
TOYOMURA K., FUJIMURA T., MURAKAMI H., NAISUME T., SHIGEHISA T., INDUE N., TAKEDA J., KINOSHITA T.;
INT. IMMUNOL. 9:869-875(1997).
EMBL; D70897; G1018989; -. SUS SCROFA (PIG). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; ä Score 77; DB 4; Length 363; Pred. No. 5.22e-02; 7; Mismatches 9; Indels RESULT
1 D 002839
AC 002839; TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SHOUTHON UPDATE)
DE PORCINE MEMBRANE COFACTOR PROTEIN. 363 AA; 39692 MW; AD14F57A CRC32; 98 PLQEACRRKACS-NLPDPLNGQVSYPNG 124 y Match Local Similarity 39.3%; hes 11; Conservative EUTHERIA; ARTIODACTYLA SEQUENCE Query Match MEMBRANE Matches 셤

2 PLPDCCRQKTCSCRLYELLHGAGNHAAG 29 ð

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WATERSTON R.;
                                        RESULT 9
ID 001969
AC 001969;
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Q91493
Q91493;
                                                             ID DAT THE BEAR AND THE BEAR AN
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SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING
OF DOUBLE-STRANDED DAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POIRIER F., CHAN C.T.J., TIMMONS P., ROBERTSON E.J., EVANS M.J. RIGBY P.W.J.;
DEVELOPMENT 113:1105-1114(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; RODENTIA.
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                                                                                                  Score 73; DB 3; Length 1876;
Pred. No. 2.65e-01;
5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 72; DB 9; Length 815;
Pred. No. 3.94e-01;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 72; DB 10; Length 147
Pred. No. 3.94e-01;
9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYXOCOCCUS XANTHUS.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; MYXOBACTERALES;
MYXOCOCCACEAE.
                                                                                                                                                                                                                                                                                                                                                                           LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                             DF107ECF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ000543; E1168188; -.
PROSITE; PS00177; TOPOISOMERASE_II; 1.
ISOMERASE; TOPOISOMERASE; AIP-BINDING.
SEQUENCE 815 AA; 89636 MW; 65A25520 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X58196; G51133; -...
SEQUENCE 147 AA; 16309 MW; 6DC857F5 CRC32;
                                                                                                                                                                                                                                                                                                                   Æ
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                                                                                                                                                                                                                                                                                                                   147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 CCRQKTCSCRLYELLHGAGNHAAGILTL 33
J. BIOL. CHEM. 271:13892-13899(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 CCNQNHYTTCLRNLLQGEAERTDGVNIL 93
                                                                                                                                                                                                                                                                                                                                                         CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                     501 RRKTCT-RLYELISDQRTDDPELL 523
                 EMBL; U52192; G1272420; --
FLYBASE; FBGN0015278; P13K6BD.
SEQUENCE 1876 AA; 210505 MW;
                                                                                                                                                                                                               691 PSCRRRSTWSCRLCAEHLRGAG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 PDCCRQKTCSCRLY-ELLHGAG 24
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01-NOV-1996 (TREMBLREL. 01,
01-NOV-1996 (TREMBLREL. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.1%;
ilarity 32.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.1%;
Best Local Similarity 59.1%;
Matches 13; Conservative
                                                                                                                         Best Local Similarity 41.7%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
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01-JAN-1998 (TREMBLREL.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C57B1/6;
MEDLINE; 92249159.
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                                                                                                        Query Match
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033367
033367;
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Q61639
Q61639;
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WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BEEKS M.,
WILSON R., AINSCOUGH R., COPSEY T., COOPER J., COULSON A.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
GARDNER A., GREEN P., HAWINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
SMALDON J., PERCY C., MCMORRAY A., MORTIMORES B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFER L., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WAITERSTON R.,
WAITSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                           EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA
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EUTARRYOTA, METALOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
CHONDRICHTHYES.
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Pred. No. 8.65e-01;
....matches 7; Indels
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GATTUNG S., GOELA D., WILSON R.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBMITTED (MAX-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF003739; G2105488; -
PROSITE; PS00627; GHMS-KINASES_ATP; 1.
SEQUENCE 426 A43, 47290 MW; 7CBEF743 CRC32;
                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
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MEDLINE; 92064638.
TEADON J.E., LIN H., DYER S.M., BURDEN S.J.;
J. CELL BIOL. 115:1069-1076(1991).
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J. PHYSIOL. (PARIS) 0:131-133(1991).
EMBL. M37645; G397971; -.
PROSITE: PS01159; WW_DOMAIN_1: 1.
NON_TER
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PRT;
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                                                    01-JUL-1997 (TREMBLREL. 04, 01-JUL-1997 (TREMBLREL. 04, 01-JAN-1998 (TREMBLREL. 05, SIMILAR TO GALACTOKINASE.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 27.3%;
Best Local Similarity 48.1%;
Matches 13; Conservative
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MEDLINE; 94150718.
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O; Gaps
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01-NOY-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOY-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
KAPS.5 KERATIN PROTEIN (FRAGMENT).
KRTAPS.5.
KRTAPS.5.
EUTHER S. SHEEP).
EUTHERIA; METALOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                   Score 66; DB 9; Length 479;
Pred. No. 3.99e+00;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 65; DB 4; Length 197;
Pred. No. 5.80e+00;
2; Mismatches 3; Indels
STRAIN-168;
KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; 299106; E1182356; -.
SEQUENCE 479 AA; 55166 MW; 3C2D1F5A CRC32;
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TISSUB-WOOL FOLLICLE;
MEDLINE; 94384466.
JENNEST. DERMATOL. 103:310-317(1994).
EMBL; X73435; G313722; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.4%;
Best Local Similarity 58.3%;
Matches 7; Conservative
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Best Local Similarity 41.2%;
Matches 7; Conservative
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15 RLYELLHGAGNHAAGIL 31
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Q28584
Q28584;
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arch completed: Thu Jul 30 09:31:53 1998 time: 25 secs.

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Release 3.1A John F. Collins, Blocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:23:30 1998; MasPar time 4.56 Seconds 216.418 Million cell updates/sec bular output not generated.

>US-08-938-548A-9 (1-27) from USO8938548A.pep 192 1 PGPPGLQGRLQRLLQANGNHAAGILIM 27 Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

120441 seqs, 36531193 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d Database:

Mean 29.905; Variance 54.628; scale 0.547 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Drod		5.23e+00	5.23e+00	7.27e+00	7.27e+00	7.27e+00	7.27e+00	7.27e+00	7.27e+00	7.27e+00	7.27e+00	7.27e+00	1.01e+01	1.01e+01	1.01e+01	1.39e+01	1.39e+01	1.91e+01	1.91e+01	1.91e+01	1.91e+01	1.91e+01	1.91e+01	2.62e+01
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	£		S47044	H64888	E69913	A41654	B41654	JH0496	S11712	S41307	JN0443	JN0445	A55152	D69081	S49183	S19248	A33988	G01880	S25618	S51155	A46101	B46101	RDYCS7	S64616	S61858
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#journal Science (1997) 277:1453-1462
#title The complete genome sequence of Escherichia coli K-12.
#cross.references MUID:97426617
#accession H648B preliminary; nucleic acid sequence not shown:

32.8 556 2 B64939 hypothetical protein 2.62e+01 32.8 770 2 S77523 hypothetical protein 2.62e+01 32.8 770 2 S77523 hypothetical protein 2.62e+01 32.8 878 2 A41055 ecdysone receptor - f 2.62e+01 32.3 36 2 B49139 allergen TBR-1 - Toxo 3.59e+01 32.3 33.1 2 S7765 hypothetical protein 3.59e+01 32.3 380 2 S76929 hypothetical protein 3.59e+01 32.3 400 2 S76929 hypothetical protein 3.59e+01 466 2 S61292 transcription initiat 3.59e+01 47076 collagen alpha 1(VII) 3.59e+01 52.3 1690 1 CGHUIB collagen alpha 1(VII) 3.59e+01 collagen alpha 4(IV) 3.59e+01 1763 2 S1636 collagen alpha 4(IV) 3.59e+01 hypothetical protein 4.89e+01 hypothetical hypothetical hypothetical hypothet	S47044 mALDP pp #formall 13-Jan-10-Se S47044 S47044 SA7044 Sarde, CDNA se adren S47044 E_TYPE MR. S47044 SA7044	tch 35.4%; Score 68; DB 2; Length 736; al Similarity 44.4%; Pred. No. 5.23e+00; 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0; aGIPKWQGRLQELRQILGEAAAPVQPL 730 :	H64888 #type complete hypothetical protein b1381 - Escherichia coli (strain K-12) #formal_name Escherichia coli 12.5ep-1997 #sequence_revision 17.5ep-1997 #text_change 14.4888 464720 Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
22 25 25 25 26 25 26 26 26 26 26 26 26 26 26 26 26 26 26	RESULT 1 TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors #submission #description #description #accession	Query Match Best Local S. Matches 1: Db 704 AGIPI Qy 1 PGPPR	RESULT 2 ENTRY TITLE TITLE DATA ACCESSIONS REFERENCE #authors

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Gaps

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Indels

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Best Local Similarity 31.8%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                             ##molecule_type DNA
##residues 1.442 ##label SHI
##cross-references EMBL:X52983
##note the authors translated the codon CAG for residue 430 as
##note His and GGG for residue 431 as Pro
NT This protein is the functional homolog of the principal sigma
factors involved in the transcription of housekeeping genes.

    Streptomyces

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription initiation factor sigma hrdB - Streptomyces
                                                                                                                                                                                Shiina, T.; Tanaka, K.; Takahashi, H. Gene (1991) 107:145-148
Sequence of hrdB, an essential gene encoding sigma-like
transcription factor of Streptomyces coelicolor A3(2):
homology to principal sigma factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #superfamily transcription initiation factor sigma katf; transcription initiation factor sigma katf homology
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                                                                sigma-like transcription factor
#formal_name Streptomyces coelicolor
31.Mar-1992 #sequence_revision 31.Mar-1992 #text_change
24.Jul-1997
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03-May-1994 #sequence_revision 20-Feb-1995 #text_change
08-Sep-1997
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#length 442 #molecular-weight 48364 #checksum 4785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA binding; sigma factor; transcription initiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, May 1990
Multiple homolog genes for principal sigma subunit
Streptomyces coelicolor A3(2).
                    JH0496 #type complete
transcription initiation factor sigma homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 442;
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##experimental_source strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tanaka, K.; Shiina, T.; Takahashi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l. No. 7.27e+00;
Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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#contents A3[2]
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Best Local Similarity 31.8%;
Matches 7; Conservative
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##residues 1-44
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#description
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ORGANISM
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#title
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S41307 #type complete transcription initiation factor sigma - Streptomyces griseus #formal_name Streptomyces griseus 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
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Gene (1992) 122:63-70
Four genes in Streptomyces aureofaciens containing a domain
characterstic of principal sigma factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marcos, A.T.; Diez, B.; Gutierrez, S.; Fernandez, F.J.; Velasco, J.; Martin, J.F. submitted to the EMBL Data Library, December 1993 organization and expression of the hrdb-sprC gene cluster o streptomyces griseus encoding a signa factor protein and serine protease. Role on growth and sporulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *superfamily transcription initiation factor sigma katF;
transcription initiation factor sigma katF homology
DNA binding; sigma factor; transcription initiation
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transcription initiation factor sigma katF homology
DNA binding; sigma factor; transcription initiation
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Streptomyces aureofaciens
*formal_name Streptomyces aureofaciens
30-Sep-1993 *sequence_revision 30-Sep-1993 *text_change
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homology #label KTF
#length 525 #molecular-weight 57204 #checksum 9676
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#length 510 #molecular-weight 55795 #checksum 1415
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##cross-references EMBL:X75952; NID:9440164; PID:9581664
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Pred. No. 7.27e+00;
11; Mismatches 4; Indels
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##cross-references GB:M90411; NID:g153305; PID:g153306
Pred. No. 7.27e+00;
11; Mismatches 4;
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LQGRLQRLLQANGNHAAGILIM 27
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Best Local Similarity 31.8%;
Matches 7; Conservative
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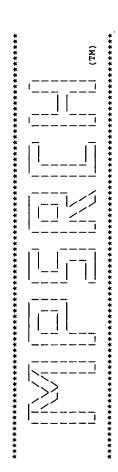
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CLASSIFICATION
                                        ##status
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1328-1413
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                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors Herzer, P.J.; Inouye, S.; Inouye, M.
#journal Mol. Microbiol. (1992) 6:345-354
#title Retron Ec107 is inserted into the Escherichia coli genome by replacing a palindromic 34bp intergenic sequence.
#cross-references MUID:92204001
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Adenylate cyclases in yeast: a comparison of the genes from Schizosaccharomyces pombe and Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                     S19248 #type complete
RNA-directed DNA polymerase (EC 2.7.7.49), msDNA specific
Escherichia coli retron Ecl07
DNA nucleotidyltransferase (RNA-directed); reverse
transcriptase; revertese
#formal_name Escherichia coli retron Ecl07
20.Feb-1995_#sequence_revision 15-Oct-1996 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:7989-7993
#title The adenyly1 cyclase gene from Schizosaccharomyces pombe.
#cocession A33988
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#formal_name Schizosaccharomyces pombe
23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change
09-Sep-1997
                                                                                                  Gaps
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#superfamily reverse transcriptase
nucleotidyltransferase
#length 319 #molecular-weight 36363 #checksum 2019
##cross-references EMBL:X79980; NID:9510451; PID:9510452
Y #Length 253 #molecular-weight 27305 #checksum 1526
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                                                    Score 66; DB 2; Length 253;
Pred. No. 1.01e+01;
5; Mismatches 10; Indels
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##experimental_source E. coli wild strain
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Pred. No. 1.01e+01;
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ilarity 37.5%;
Conservative
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Best Local Similarity 50.0%;
Matches 9; Conservative
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Gaps
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homology #label YACC
#length 1692 #molecular-weight 190332 #checksum 2609
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Pred. No. 1.39e+01;
3; Mismatches 3; Indels
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#cross-references MUID:89345533
#accession A33539
                              preliminary
                                                                                                                                                                                                                                 33.9%;
llarity 57.1%;
Conservative
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Best Local Similarity
Matches 8; Conserv
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Job time: 13 secs.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 09:24:01 1998; MasPar time 4.11 Seconds 164.767 Million cell updates/sec bular output not generated. :uo u

>US-08-938-548A-9 (1-27) from US08938548A.pep 192 1 PGPPGLQGRLQRLLQANGNHAAGILIM 27 Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

69111 seqs, 25083644 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

swiss-prot35 1:swiss1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 31.311; Variance 47.835; scale 0.655

#### SUMMARIES

Result No.	Score	% Query Match	% Query Match Length	DB	<b>1</b>	Description	Pred. No.
-	68	35.4	736	<u> </u>	ALD MOUSE	ADRENOLEUKODYSTROPHY P	1.44e+00
7	99	35.4	879	Н	YDBH_ECOLI	HYPOTHETICAL 96.8 KD P	1.44e+00
m	67	34.9	187	-	SODC_HAEPA	SUPEROXIDE DISMUTASE P	2.09e+00
4	67	34.9	187	М	SODC_HAEIN	SUPEROXIDE DISMUTASE L	2.09e+00
ហ	67	34.9	442	Н	HRDB_STRCO	RNA POLYMERASE PRINCIP	2.09e+00
9	67	34.9	1157	1	PEX1_PICPA	PEROXISOME BIOSYNTHESI	2.09e+00
7	65	33.9	307	Н	CC36_CAEEL	CUTICLE COLLAGEN 36.	4.39e+00
œ	65	33.9	1692	н	CYAA_SCHPO	ADENYLATE CYCLASE (EC	4.39e+00
6	65	33.9	1992	<del>,1</del>	TR12_HUMAN	THYROID RECEPTOR INTER	4.39e+00
10	64	33.3	199	ч	IL11_MOUSE	INTERLEUKIN-11 PRECURS	6.32e+00
11	64	33.3	624	Н	SIR_SYNP7	SULFITE REDUCTASE (FER	6.32e+00
12	64	33.3	1477		YOR1_YEAST	OLIGOMYCIN RESISTANCE	6.32e+00
13	63	32.8	702	H	YCBY_ECOLI	HYPOTHETICAL 78.9 KD P	9.05e+00
14	63	32.8	878	H	ECR_DROME	ECDYSONE RECEPTOR (ECD	9.05e+00
15	62	32.3	256	Н	YREC_SYNP2	HYPOTHETICAL 28.7 KD P	1.29e+01
16	62	32.3	380	М	F812_MOUSE	FACTOR VIII INTRON 22	1.29e+01
17	62	32.3	400	Н	ASSY_SYNY3	ARGININOSUCCINATE SYNT	1.29e+01
18	62	32.3	652	Н	RPSD_CAUCR	RNA POLYMERASE SIGMA F	1.29e+01
19	62	32.3	1690	Н	CA44_HUMAN	COLLAGEN ALPHA 4(IV) C	1.29e+01
	62	32.3	1758	-	CA24_CAEEL	COLLAGEN ALPHA 2(IV) C	1.29e+01
21	62	32.3	1763	٦	CA24_ASCSU	PROCOLLAGEN ALPHA 2(IV	1.29e+01
22	61	31.8	134	Н	Y652_METJA	HYPOTHETICAL PROTEIN M	1.83e+01
23	61	31.8	180	Н	NEF_HV2NZ	NEGATIVE FACTOR (F-PRO	1.83e+01

1.83e+01 1.83e+01 1.83e+01 1.83e+01	1.83e+01 1.83e+01 1.83e+01	1.83e+01 1.83e+01 2.59e+01	2.59e+01 2.59e+01 2.59e+01	2.59e+01 2.59e+01 2.59e+01	2.59e+01 2.59e+01 2.59e+01
TRANSCRIPTIONAL REGULA HYPOTHETICAL OXIDOREDU PULMONARY SURFACTANT-A HYPOTHETICAL 28 KD PROCOAT PROTETN VP1	BETA-ARRESTIN 2. BETA-ARRESTIN 2 (ARRES PROTEIN UL88.	PHEROMONE B ALPHA 2 RE PROBABLE DNA PACKAGING INTERLEUKIN-11 PRECURS	CARBAMOYL-PHOSPHATE SY HYPOTHETICAL 45.5 KD P BETA-ARRESTIN 2. COLLAGEN ALPHA 1 (VIII)	COLLAGEN ALPHA 1(VIII) ACONITATE HYDRATASE, M REGULATORY PROTEIN ALC	COENZYME POO SYNTHESIS COLLAGEN ALPHA 1(XI) C HC-TOXIN SYNTHETASE (E
BASR_SALTY YDGB_ECOLI PSPA_HUMAN YPE1_RHORU	ARRZ_HUMAN ARRZ_BOVIN UL88_HCMVA	BAR2_SCHCO VTER_EBV IL11_HUMAN	CARA_PSEAE YL37_CAEEL ARR2_RAT	CA18_RABIT ACON_BOVIN ALCR EMENI	POOF_PSEFL CA1B_HUMAN HTS1_COCCA
	4-	. – – –		1444	
225 240 255 255 255	4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	518 690 199	378 400 410 743	744 780 821	829 1806 5217
311.8	311.8	31.8	31.3	1	31.3 31.3
16611	1000	61 61 60	0000	0000	000
225 225 24 27	33028	. w w w 1 w 4 w	33.37 28.00 30.00	9444 0016	4 4 4 6 4 6

### ALIGNMENTS

10; 5; Mismatches 704 AGIPKMQGRLQELRQILGEAAAPVQPL 730 1 PGPPGLQGRLQRLLQANGNHAAGILTM 27 12; Conservative Matches 쉱 ò

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879 AA. PRT; RESULT 2 ID YDBH\_ECOLI STANDARD; AC P52645; P77502; P76855;

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Gaps

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P18183

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RESULT
1D HF
DT 011
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-1- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE PROPEINS. THE CITICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A BARKIER TO PROTECT THE WORM FROM ITS ENVIRONMENT.
-1- SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYAA_SCHPO STANDARD; PRT; 1692 AA.
P14605;
01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-EB-1996 (REL. 33, LAST ANNOTATION UPDATE)
ADENTLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).
CYRIL.
                                                                                                                                                                                                                                                                                                                                                                     CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT; MULTIGENE FAMILY; COLLAGEN.
TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: TO OTHER COLLAGENS. STRONG, TO OTHER CUTICLE COLLAGENS.
EMBL: 115418; 0289662; -.
EMBL: U16435; G540271; ALT_INIT.
HSSP; P02462; 1BBE.
                                                                               Score 67; DB 1; Length 1157;
Pred. No. 2.09e+00;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAULEY A.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
                                                MW; 3FBC3905 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 4.39e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9346DA48 CRC32;
                                                                                                                                                                                                                                                                                01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
CUTICLE COLLAGEN 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
               (POTENTIAL)
                                (POTENTIAL)
                                                                                                                                                                                                                                                     307 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 65;
                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150
187
226
17
257
17
295
30126 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WORMPEP; C27H5.5; CE06893.
CUTICLE; CONNECTIVE TISSUE;
                                                126984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.98;
55.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 PGPPGPAGQPGRVIQVNG 231
                                                                             34.9%;
Similarity 60.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PGPPGLQGRLQRLLQANG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
                                                                                                                                                  1072 KLEHLYQGNGNHAEG 1086
                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                     KRAMER J.M.;
             530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEVY A.D., KRAMER J.M.;
GENE 137:281-285(1993).
             523 53
840 84
1157 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 :
                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
MEDLINE; 94131298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       COL-36 OR C27H5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                   CC36_CAEEL
P34803;
             NP_BIND
NP_BIND
SEQUENCE
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MEDLINE; 89058616.
TANAKA K., SHIINA T., TAKAHASHI H.;
SCIENCE 242:1040-1042(1988).
-: FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEYMAN J.A., MONOSOV E., SUBRAMANI S.;
J. CELL BIOL. 127:1259-1273(1994).
-!- FUNCTION: INVOLVED IN PEROXISOME BIOSYNTHESIS. MAY PLAY A DIRECT OR INDIRECT ROLE IN DELIVERING MEMBRANE MATERIAL TO DEVELOFING PEROXISOMES. IT MAY ALSO BE INVOLVED IN INTRACELLULAR MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X52983; G48745; -.
PIR; S11712; S11712.
PROSITE; PS00715; SIGMA70_1; 1.
PROSITE; PS00715; SIGMA70_2; 1.
TRANSCRIPTION REGULATION; SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 246 POLYMERASE CORE BINDING (POTENTIAL).
403 422 H-T-H MOTIF (BY SIMILARITY).
442 AA; 48413 MW; 4720321F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   THEN IS RELEASED.
-!- SIMILARITY: TO OTHER SIGMA FACTORS THAT DO NOT BELONG TO THE SIGMA-54 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                     PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLUIAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
EMBL: 236897; G537420; -.
PROSITE; PSO0674; AAA; 1.
Pred. No. 2.09e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PEROXISOME BIOSYNTHESIS PROTEIN PASI (PEROXIN-1).
PEXI OR PASI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 67; DB 1; LA Pred. No. 2.09e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                   01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                     442 AA
                                                                                                                                                                                                                                                   RNA POLYMERASE PRINCIPAL SIGMA FACTOR HRDB
                                                                 30 PAGPSIEVKVQQLDPANGNKDVGTVTI 56
                                                                                                1 PGPPGLQGRLQRLLQANGNHAAGILTM 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEROXISOME; ATP-BINDING; REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 LQEQLHSVLDTLSEREAGVVSM 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.9%;
llarity 31.8%;
Conservative
               Best Local Similarity 37.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                      STREPTOMYCES COELICOLOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PICHIA PASTORIS (YEAST)
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Best Local Similarity
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MEDLINE; 95050987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-BINDING
                                                                                                                                                                  HRDB_STRCO
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P46463;
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SEQUENCE
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STRAIN-K12 / MG1655;
STRAIN-K12 / MG1655;
STRAIN-K12 / MG1655;
STRAIN-K12 / MG1655;
BLAITNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
--- SIMILARITY: TO B.SUBTILIS YWBD.
--- SIMILARITY: TO B.SUBTILIS YWBD.
--- SIMILARITY: BELONGS TO THE UPF0020 FAMILY.
EMBL, AE000197; G1787181;
--- ECOGENE; EG1377; YCBY.
PROSITE; PS010261; UPF0020; 1.
PROSITE; PS01092; NG_MTASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESCHERICHIA COLI.
PROKARYOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
VOLCKAERT G., VOET M., ROBBEN J.;
YEAST 13:521-256(1997).
-1- FUNCTION: REQUIRED FOR OLIGOMYCIN RESISTANCE.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- SUBILARITY: BELONGS TO THE ATP-BINDING TRANSFORT PROTEIN FAMILY.
CARC TRANSPORTERS). BELONGS TO THE MDR SUBFAMILY.
SED: LO003083; YOR1.
SGD; LO003083; YOR1.
SGD; LOO03083; YOR1.
PROSTIE; PSO0211, ABC_TRANSPORTER; 1.
TRANSMEM 207 227 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 78-9 KD PROTEIN IN PYRD-PQIA INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 64; DB 1; Length 1477;
Pred. No. 6.32e+00;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79B302B8 CRC32;
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Pred. No. 9.05e+00;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          702 AA; 78854 MW; 3218A412 CRC32;
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GRLQRLLQANGNHAAGILTM 27
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larity 61.5%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 33.3%;
Best Local Similarity 40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                           636
913
913
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628
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1366 136
1477 AA;
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Best Local Similarity
Matches 8; Conserv
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YCBY_ECOLI
P75864;
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CARBOHYD
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TRANSMEM
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         SO THE FERTHER FERTHER SO THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 93349955.

A GISSELMANN G., KLAUSMEIER P., SCHWENN J.D.;
BIOCHTH. BIOPHYS. ACTA 1144:102-106(1993).

C -!- CATALYTIC ACTIVITY: 4(2)S + 3 OXIDIZED FERREDOXIN + 3 H(2)O = SULFITE + 3 REDUCED FERREDOXIN.

-!- COFACTOR: THIS ENZYME CONTAINS ONE SIROHEME AND ONE 4FE-4S IRON-SULFUR CENTER AS PROSTHETIC GROUPS.

-!- SUBUNIT: MONOMER AS PROSTHETIC GROUPS.

-!- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN FOUND IN NITRITE REDUCTASES (EC 1.6.6.4 AND EC 1.7.1) AND SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).

R EMBL; 211755; G38930; --

R PIR; S19860; RDYCS7.
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RATZHAND DJ., HALLSTROM T.C., VOET M., WYSOCK W., GOLIN J., VOCKRAERT G., MOYL-ROWLEY W.S.;
MOL. CELL. BIOL. 15:6875-6883(1995).
                                                                                                                                                                                                                                                                                                                                                                                                   SYNECHOCOCCUS SP. (STRAIN PCC 7942) (ANACYSTIS NIDULANS R2) PROKARYOTA; GRACILICUTES; OXYPHOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 64; DB 1; Length 624; Pred. No. 6.32e+00;
       DB 1; Length 199;
6.32e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
0LIGOMYCIN RESISTANCE ATP-DEPENDENT PERMEASE YORI.
                                                                                                                                                                                                                                                                                                                                                                                                                        PROKARYOTA; GRACILICUTES; OXYPHOYUBACIBAIA;
CYANOBACIBRIA (BLUE-GREEN ALGAE); CHROOCOCCALES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                 01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
SULFITE REDUCTASE (FERREDOXIN) (EC 1.8.7.1).
                                                    4; Mismatches
                                                                                                                                                                                                                                        624 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1477 AA
       Score 64;
Pred. No. (
                                                                                                                                                                                                                                        PRT;
    33.3%;
Similarity 53.3%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.3%;
Similarity 53.3%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464 PGLLVRIRRLLEEQG 478
                                                                                                 124 PELGALQARLERLLR 138
                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                         | :||:||:||:
1 PGPPGLQGRLQRLLQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 PGLQGRLQRLLQANG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-S288C / FY1679;
MEDLINE; 97245295.
       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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P53049;
                                                                                                                                                                                                                                      SIR_SYNP7
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Gaps

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702 AA

Matches

RESULT

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Gaps

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Length 702; 2; Indels US-08-938-548A-9.rspt

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 09:24:28 1998; MasPar time 5.15 Seconds 220.864 Million cell updates/sec MPsrch\_pp : uo d

abular output not generated.

>US-08-938-548A-9 (1-27) from US08938548A.pep 192 1 PGPPGLQGRLQRLQANGNHAAGILIM 27 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

140542 seqs, 42109429 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl5
1:sp\_fungi 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Mean 29.753; Variance 52.286; scale 0.569 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Query Match Length DB
1277
249
1174
178
46
21
514
525
528
568
809
130
150
253
304
319
377
1465
580
1344

1.15e+01 1.60e+01 1.60e+01 1.60e+01	1.60e+01 1.60e+01 2.22e+01	2.22e+01 2.22e+01 2.22e+01	3.08e+01 3.08e+01 3.08e+01 3.08e+01	3.08e+01 3.08e+01 3.08e+01 3.08e+01	3.08e+01 3.08e+01 4.24e+01 4.24e+01
FATTY ACID SYNTHASE (E PUTATIVE SIGMA-54 DEPE ORE263 HOMODA HYDROLASE.	PROTEIN TYROSINE PHOSP KM-102-DERIVED REDUCTA HRPE.	FROM BASES 1860594 TO NODO. HYPOTHETICAL 85.5 KD P KTAA0310	GMENT) NSFERA CAL 37	KNA POLYMERASE SIGMA F. C-SRC TYROSINE KINASE. RNA POLYMERASE SIGMA F. TYPE VII COLLAGEN (FRA COLLAGEN A1 XIX CHAIN.	CODED FOR BY C. ELEGAN C. ELEGANS COLLAGEN AL RETINA SPECIFIC RGS PR TRANSCRIPTIONAL ACTIVA
Q16702 Q50872 Q31722 Q51980	027932 099475 052495	P76237 007309 P73339	P96282 032855 P74570 Q19452	059552 059532 063870 035053	Q19098 Q19099 P79348 Q51454
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2509 140 263 288 288	548 439 99	556 633 770 881	3310 3310 457	527 527 574 920 1136	1758 1759 374 473
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2222 2222 243	226	330	1 W W W W W	2 8 8 4 4 7 8 9 0 1	4 4 4 4 2 6 4 2

## ALIGNMENTS

		Gaps	
MAMMALIA;		Length 1277;	MAMMALIA;
PRT; 1277 AA. CREATED) LAST SEQUENCE UPDATE) LAST ANNOTATION UPDATE) ; VERTEBRATA; TETRAPODA;	DBJ DATA BANKS.	75; DB 10; Length No. 3.48e-01; Mismatches 5; Ind 852	A. UPDATE) N UPDATE) TETRAPODA;
Æ	SCHIBLER U.; EMBL/GENBANK/DDBJ  675 MW; 89721F79	0) •	PRT CREAT LAST LAST A; VER
	U.; 190). V., TO 111; 144	39.1%; Scor. al Similarity 29.6%; Pred 8; Conservative 14; PGAEALHAQVERFVQQAGNQADASVAL   :: :::: ::    : ::::	PRELIMINARY; 77 (TREMBLREL. 03, 77 (TREMBLREL. 03, 77 (TREMBLREL. 03, BETA4 SUBUNIT. US (MOUSE). METAZOA; CHORDAT. RODENTIA. RODENTIA.
11. 1 PRELIMIN 035821 035821 035821 015821 01-3AN-1998 (TREMBLREL. 01-3AN-1998	BIEL ERIE	Query Match Best Local Simi. Matches 8; 826 PGAEALH 1 PGPPGLQ	2 97382; 97382; 1-MAY-1997; 1-MAY-1997; 1-MAY-1997; 1-MAY-1997; 1-MAY-1997; 1-MARYOTA; UTHERIA; EQUENCE FF
RESULT ID AC AC OO DI DO DI DO DE P P OC E E	S D R R R R R R R R R R R R R R R R R R	D DD ME	RESULT 1D PO 1D DT DT O O DT O

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KORMANEC J., FARKASOVSKY M., POTUCKOVA L.;
GENE 122:63-70(1992).
-1- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
THEN IS RELEASED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M90411; G153306; -.
PROSITE; PS00715; SIGMA70_1; 1.
PROSITE; PS00716; SIGMA70_2; 1.
TRANSCRIPTION REGULATION; SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE;
                                                                                                                                                                                                                                                     PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.
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pred. No. 5.84e+00;
9; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                            CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 67; DB 9; LA
Pred. No. 5.84e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 525 AA; 57204 MW; 7B7689F1 CRC32;
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                                               525 AA
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Q27212
Q27212;
Q1-NOV-1996 (TREMBLREL. 01, CREATED)
                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       453 LQEQLHSVLDTLSEREAGVVSM 474
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          ULT 8
059813
059813;
01-NOV-1996 (TREMBLREL. 01, C1)
01-NOV-1996 (TREMBLREL. 01, LA)
01-JAN-1998 (TREMBLREL. 05, LA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.9%;
ilarity 31.8%;
Conservative
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6 LOGRLORLLQANGNHAAGILTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 36.4%;
Matches 8; Conservative
                                                                                                                                                                              RNA POLYMERASE SIGMA FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREPTOMYCES AUREOFACIENS
                                                                                                                                                                                                                                STREPTOMYCES AUREOFACIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 93083996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              059814
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ID 02
AC 02
DT 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENE 153:41-48(1995).

-1- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
THEN IS RELEASED.
EMBL; X75922; G581664; -
PROSITE; PS00715; SIGMA70_1; 1.
PROSITE; PS00716; SIGMA70_2; 1.
PROSITE; PS00716; SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHINKAWA H., HATADA Y., OKADA M., KINASHI H., NIMI O.;
J. BIOCHEM. 118:494-499(1995).
-!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
THEN IS RELEASED.
EMBL, LO8071; G1617256.
-.
PROSITE: PS00715: SIGMA70_1; 1.
PROSITE: PS00716; SIGMA70_2; 1.
TRANSCRIPTION REGULATION; SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE;
DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=IMRU 3570;
MEDLLINE: 95189101.
MARCOS A.T., DIEZ B., GUTIERREZ S., FERNANDEZ F.J., OGUIZA J.A.,
MARTIN J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREPTOMYCES GRISEUS.
PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 67; DB 9; Length 514;
Pred. No. 5.84e+00;
11; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 67; DB 9; Length 510;
Pred. No. 5.84e+00;
11; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-APR-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
RNA POLYMERASE SIGMA FACTOR.
                                                                                                                                                                                                   01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
RNA POLYMERASE SIGMA FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       510 AA; 55795 MW; C3CB64EB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               514 AA; 56132 MW; 792FDDFF CRC32;
                                                                                                                                                      510 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    514 AA
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                                                                                                                                                      PRT;
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LQEQLHSVLDTLSEREAGVVAM 411
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6 LQGRLQRLLQANGNHAAGILTM 27
                               | | | :|: :|: ::: ||:::|
6 LQGRLQRLLQANGNHAAGILTM 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 31.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 34.9%;
Best Local Similarity 31.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                               STREPTOMYCES GRISEUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA-BINDING.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                         LT 6
Q59913
Q59913;
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P77951;
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RESULT

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Gaps

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Gaps

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MEDLINE; 94150718.

MEDLINE; 94150718.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BOLFIELD J., BURTCON J., CONNELL M., COPER J., COULSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., COULSON A., CRAXTON M., RENEMA P., HALLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., ACHIAGHAN M., PARSONS J., LLOYD C., MCHURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., SONNHAMMER E., STADEN R., SUGLYON J., THERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WALLOND A., WEINSTOCK L., WHILDMAN P.;

MAILKINGON-SPROAT J., WHILDMAN P.;

MATURE 368132-38(1994).

SEQUENCE 304 AA; 34775 MW; C4AAIEFB CRC32;
                                                                                                                                           EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 304;
                                                                                                                                                                                                 WILKINSON J.;
SUBMITIED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                    01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 66; DB 3; Le
Pred. No. 8.20e+00;
7; Mismatches 6;
                  304 AA.
                  PRT;
                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 40.9%;
Matches 9; Conservative
                                                                                                           T24D5.1.
CAENORHABDITIS ELEGANS
                                                                                                                                                                              SEQUENCE FROM N.A.
O22732
Q22732;
   RESULT
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Search completed: Thu Jul 30 09:24:41 1998 Job time : 13 secs.

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Gaps

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6; Indels

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp .. 0

Thu Jul 30 09:10:49 1998; MasPar time 3.13 Seconds 137.296 Million cell updates/sec

not generated. lar output

Title: Description: Perfect Score:

>US-08-938-548A-4 (1-28) from USO8938548A.pep 196 1 RSGPPGLOGRLOAGSUHAAGILIM 28 Sequence:

PAM 150 Gap 15 Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

124785 segs, 15338987 residues

Searched:

a-geneseq31-2 Database:

| part| 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 4:part14 15:part15 16:part10 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27

Mean 21.977; Variance 87.361; scale 0.252 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

)		dФ					
Result No.	Score	Query Match	Length	DB	a	Description	Pred. No.
-	89	34.7	716		P99737	Dottonia X recentor 4	1 320+01
10	62	34.2	1477	3 6	W10424	Cadobaromyoo coronta	5 226.01
۳ ۱	7	2. 7.5	1477	9 ~	557501	Secondition Cerevis	7.226.01
•	67	34.2	1843	2 5	W22605	TVIACTORE SUNTHAGE OR	5.22e+01
. rv	67	34.2	2192	3	W21732	LexA/NuMA fusion prot	5.22e+01
9	67	34.2	2272	23	W21731	GAL4/HA/NUMA fusion p	5.22e+01
7	67	34.2	4630	22	W19629	Streptomyces venezuel	5.22e+01
80	99	33.7	10	4	R20235	"p33" N-terminal (2).	6.30e+01
σ	63	32.1	32	-1	R00579	New polypeptide based	1.10e+02
10	63	32.1	248	m	P60442	Plasmid pASPcq-SV(10)	1.10e+02
11	63	32.1	248	П	P80694	Sequence deduced from	1.10e+02
12	63	32.1		7	P70663	35kd pulmonary surfac	1.10e+02
13	63	32.1	248	Н	P82980	Sequence deduced from	1.10e+02
14	63	32.1		m	P60665	Sequence of human alv	1.10e+02
15	63	32.1	248	m	P60666	Genomic sequence of h	1.10e+02
16	63	32.1	248	-	R04216	Human 32K ASP encoded	1.10e+02
17	63	32.1	248	~	P70662	35kd pulmonary surfac	1.10e+02
18	63	32.1	248	Н	R04215	Human 32K ASP encoded	1.10e+02
19	63	32.1	248	m	P60441	Plasmid pASPc-SV(10)	1.10e+02

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1.100e 1.	1.91e+02 1.91e+02 1.91e+02 1.91e+02 1.91e+02 1.91e+02 1.91e+02 1.91e+02
Vector PSP 35K-1A-10 Human alveolar surfac Human 32K ASP encoded Genomic sequence of h Human 32K alveolar su DHR23alpha protein. Ecdysone receptor. HIV-2 provirus-encode Thermus aquaticus hea Protein (0A-519) cros Human adipogenesis in Human interleukin-11	Orotidine-57-monophos Thioredoxin-IL-11 fus E-coli thioredoxin-hu Fusion protein of IL- Rat ALT. M. tuberculosis RNA p Virulence-associated Platenolide synthase
R05091 R06331 R06331 P60661 R04212 R04212 R04212 R04213 R04328 R04328 R043202 R04336 R0436 R04336 R0	R68001 R76812 R45916 R35213 W05831 W05831 W76480 W22608
2	113 113 125 25 25
248 248 271 271 271 271 271 271 2510 2509 1178 1178 1178 1178	274 2966 2966 2966 4966 3724 3724
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## ALIGNMENTS

Retinoid X receptor (RXR) interacting protein (RIP) - useful to modulate or mediate RXR function, anti-RIP antibodies can be used to determine RIP subcellular distribution patterns
Claim 2: Page 48-50: 90pp; English.

Mouse retinoid X receptor (RXR) interacting protein RIP110 (R99737) is a candidate transcriptional co-activator. It was identified using an in vivo interaction trap system for the isolation of proteins that physically interact with RXRs, esp. with the ligand binding domain of human RXR alpha. Recombinant RIP110 can be obtd. using a cDNA clone (T31930) obtd. from a mouse liver library. RIPS (see also R99735-36 and R99738-39) can be used to modulate or mediate RXR function, and may be used therapeutically or to raise antibodies. R99737;
7-SEP-1996 (first entry)
Retinoid X receptor interacting protein RIP110.
Retinoid X receptor interacting protein; RXR; RIP; RIP110. standard; Protein; 716 AA. 18-JUL-1996. 08-DEC-1995; U16311. 13-JAN-1995; US-372652. (GEHO ) GEN HOSPITAL CORP. Chol H, Moore D, Seol W; 96-342241/34. N-PSDB; T31030 Mus sp. WO9621677-A1. Sequence R99737 RESULT 

ö Gaps ö Score 68; DB 18; Length 716; Pred. No. 4.32e+01; 6; Mismatches 4; Indels 34.7%; Similarity 44.4%; 8; Conservative Query Match Best Local Similarity Matches

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RESULT 2
ID W10424 standard; Protein; 1477 AA.
AC W10424;
W10424;
DT 18-AUG-1997 (first entry)
DE Saccharomyces cerevisiae aureobasidin resistance protien scaur2.

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misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; T68715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9200329-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-1997
                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                               Claim 15; Page 42-50; 78pp; English.

The sequences given in W21731-32 represent fusion proteins which contain NuMA (nuclear mitotic apparatus). The fusion proteins were used in the identification of NuMA interecting proteins (NIP's) (see also W21729-30). Compounds which interfere with the interaction of NuMA (w21729-30). Compounds which interfere with the interaction of NuMA (w1729-30). Compounds which interfere with the interaction of NuMA (with a known NIP are used to modulate cell division and/or proliferation. Ab, raised conventionally using NIP-1 or -2 as immunogen, are used to detect NIP (or their complexes) and to block their activity for detect in the complexes and to block their activity for their complexes and to block their activity for their aberrant (including malignant) cell growth (which can also be detected by nucleic acid sequencing). Also where malignancy is related to defects in NuMA or NIP, it can be treated by administration of the appropriate functional protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences given in W2171.32 represent fusion proteins which contain NWAA (nuclear mitotic apparatus). The fusion proteins were used in the identification of NUMA interecting proteins (NIP's) (see also W21729-30). Compounds which interfere with the interaction of NUMA with a known NIP are used to modulate cell division and/or proliferation. Ab, raised conventionally using NIP-1 or -2 as immunogen, are used to detect NIP (or their complexes) and to block their activity for diagnostic or therapeutic use, e.g. to detect defective NUMA or NIP which may be markers for aberrant (including malignant) cell growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W21731;
01-0CT-1997 (first entry)
6AL4/ANWA fusion protein.
6AL4/ANWA fusion protein.
NIP-1; NIP-2; NUMA; nuclear mitotic apparatus; NUMA interacting protein;
cell division; proliferation; antibody; Ab; detection;
malignant cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                             New nucleic acid encoding nuclear mitotic appts. Interacting proteins – useful for modulating cell division and proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding nuclear mitotic appts. Interacting proteins – useful for modulating cell division and proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 67; DB 23; Length 2192;
Pred. No. 5.22e+01;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175..2272
/label= Residues_18-2116_of_NuMA
365..1864
/label= Colled_coil_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ...147
'label= GAL4_DNA_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- Hemaglutinin_epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; Page 28-36; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W21731 standard; Protein; 2272 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.2%;
larity 52.9%;
Conservative
                                                                     McPherson SMG, Snyder MP;
WPI; 97-077270/07.
N-PSDB; T77783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 838 ragrkglearlqqlgea 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McPherson SMG, Snyder MP; WPI; 97-077270/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RSGPPGLQGRLQRLLQA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148..174
                                07-JUN-1995; US-478408.
(UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-DEC-1996.
07-JUN-1996; U09504.
07-JUN-1995; US-478408.
(UYXA ) UNIV YALE.
                 07-JUN-1996; U09504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; T77782
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                                                                                                                                                                    in diagnosis
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Matches
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Industrial use

Claim 55; Fig 23; 91pp; English.

Solypeptide sequences (W19629-30 and W00918) can be deduced from
3 Polypeptide sequences (W19629-30 and W00918) can be deduced from
4 the vep ORF1 polyketide synthase (PKS) gene cluster (T68715) of
5 streptomyces venezuelae. The sequence data indicate that the PKS
5 gene cluster encodes a polyene of 12 carbons. The vep gene cluster
6 contains 5 PKS modules, plus a 5' loading module and a 3' end
7 contains 5 PKS modules, plus a 5' loading module and a 3' end
8 contains 5 PKS modules, plus a 5' loading module and a 3' end
8 contains 5 PKS modules, a keto-reductase and an acyl carrier
8 protein domain. A novel expression cassette encoding the first
8 protein domain. A novel expression cassette encoding the first
8 module from the vep gene cluster and module 7 from the Streptomyces
8 cylly gene cluster has polyhydroxyalkanoate (PHA) monomer synthase
8 activity and can be used for PHA prodn. in host (esp. insect) cells
9 for use as a biodegradable polymer.
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(which can also be detected by nucleic acid sequencing). Also where malignancy is related to defects in NuMA or NIP, it can be treated by administration of the appropriate functional protein.
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                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                ö
                                                                                                                                                        Length 2272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4630;
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Pred. No. 5.22e+01;
9; Mismatches 7; Indels
                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces venezuelae pólyketide synthase.
Polyketide synthase; polyhydroxyalkanoate monomer syn
polyhydroxybutyrate; biodegradable polymer; vep gene;
                                                                                                                                                  Score 67; DB 23; I
Pred. No. 5.22e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - see CC
                                                                                                                                                                                                                5; Mismatches
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24-APR-1992 (first entry)
"p33" N-terminal (2).
MAP; lymphocyte; IL-2; CTL; polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
ID W19629 standard; Protein; 4630 AA.
AC W19629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xue Y;
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R20235 standard; Protein; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.2%;
Local Similarity 33.3%;
hes 8; Conservative
                                                                                                                                                  Query Match
Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-008-1997.
18-DEC-1996; U20119.
19-DEC-1995; US-008847.
(MINU ) UNIV MINNESOTA.
Sherman DH, Williams MD,
                                                                                                                                                                                                                                                                           918 ragrkglearlqqlgea 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                   1 RSGPPGLQGRLQRLLQA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces venezuelae.
WO9722711-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JAN-1992.
27-JUN-1991; U04588.
27-JUN-1990; US-544862.
(BIOG-) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metabolic engineering.
                                                                                             2272 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 97-341701/31.
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Recombinant alveolar surfactant protein - used for treating respiratory distress syndrome and related diseases e.g. pneumonia and bronchitis.

Disclosure; pp; English.

The sequence was deduced from clone pHS10-4, isolated from a busclosure pp; English.

The protein is part of the alveolar surfactant protein, high mol. wt, hydrophilic 32K gp. The protein differs at 7 positions from a previously published (WO8603408) sequence, and also at several places from two other sequences cetermined by others. It is believed that the 32K human ASP protein may be encoded by multiple genes. The recombinant protein can be used for the treatment of respiratory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Regulatable expression systems - contg. human metallo:thionein-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-1991 (first entry)
Genomic sequence of human alveolar surfactant protein (hASP)
encoded by genomic DNA, used to obtain pASPcg-SV(10)
Regulatable expression system.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                   Score 63; DB 1; Length 248; Pred. No. 1.10e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Fig 5, 94pp; English.

A regulatable expression system for a coding sequence is.
The system can process genomic as well as intronless DNA.
Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-1991 (first entry)
Sequence of human alveolar surfactant protein (hASP)
on DMT(E):HS and PASPc-SV(10)
Regulatable expression system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 63; DB 3; L
Pred. No. 1.10e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-FEB-1985; US-701296.
25-NOV-1985; US-801674.
(KUSH/) BIOTECHN RES PARTNE.
(KUSH/) KUSHNER P J.
KUSHNER PJ. Cofer CL, Friedman J, Talmadge KD;
N-PSDB; N60571.
                  (CALE-) Calif Biotechn Inc.
Schilling JW, White RT, Cordell B, Benson BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 15
P60666 standard; Protein; 248 AA.
P60666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n 14
P60665 standard; Protein; 248 AA.
P60665;
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 32.1%;
Best Local Similarity 56.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.1%;
Best Local Similarity 56.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 gppglpahldeelqat 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 gppglpahldeelqat 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-FEB-1986; U00296
                                                          WPI; 88-124493/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
WO8604920-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-1986
                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter
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                                                                                                                  Disclosure: pp; English.

The sequence was deduced from clone pHS10-5, isolated from a human lung cDNA library. The protein is part of the alveolar surfactant protein, high mol. wt, hydrophilic 32K sp. The protein differs at position 50 from a previously published (W08603408) sequence, and differs at several places from two other sequences determined by others. It is believed that the 32K human ASP protein may be encoded by multiple genes. The recombinant protein can be used for the treatment of respiratory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pulmonary surfactant proteins - used for treating Hyaline Membrane Disease or Respiratory Distress Syndrome. Claim 1; Page 34A-B; 50pp; English.
                                                      Recombinant alveolar surfactant protein - used for treating respiratory distress syndrome and related diseases e.g. pneumonia and bronchitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene product may be used in treatment of Hyaline Membrane Disease
and Respiratory Distress Syndrome (RDS) in both premature infants
and adults eg. cardio-pulmonary operations. The protein products
may also be used to raise diagnostic antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-DEC-1990 (first entry)
Sequence deduced from pHS10-4, encoding human 32K ASP.
Alveolar surfactant protein; ASP; respiratory distress syndrome;
pneumonia; bronchitis; 32K.
                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-APR-1991 (first entry)
35kd pulmonary surfactant protein.
Hyaline membrane disease; respiratiory distress syndrome; RDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 63; DB 2; Length 248; Pred. No. 1.10e+02;
                                                                                                                                                                                                                                                                                                                                                                Length 248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BRIG-) Brigham and Women's Hospital.
Taeusch HW, Cobs KA, Steinbrink DR, Floros J, Phelps DS;
WPI; 87-108682/15.
                                                                                                                                                                                                                                                                                                                                                                  Score 63; DB 1; LA Pred. No. 1.10e+02;
(CALB-) Calif Biotechn Inc.
Schilling JW, White RT, Cordell B, Benson BJ;
WPI; 88-124493/18.
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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P82980 standard; protein; 248 AA.
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P70663 standard; Protein; 248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENE-) Genetics Institute Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.1%;
56.3%;
                                                                                                                                                                                                                                                                                                                                                                32.1%;
larity 56.3%;
Conservative
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26-SEP-1985; US-781130.
15-AUG-1986; US-897183.
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Pest Local Similarity
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                             Sequence
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:13:08 1998; MasPar time 1.15 Seconds 142.938 Million cell updates/sec ular output not generated. Run on:

>US-08-938-548A-4 (1-28) from US08938548A.pep 196 1 RSGPPGLOGRLOASGNHAAGILIM 28 Description: Perfect Score: Title:

Sequence:

PAM 150 Gap 15 Scoring table:

63816 seqs, 5850866 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-1ssued 1:5\_COMB 2:PCT9\_COMB 3:backfiles Database:

Mean 20.276; Variance 81.503; scale 0.249 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

•																								
	Pred. No.	1.33e+01	1.95e+01	4.17e+01	4.17e+01	6.07e+01	_	6.07e+01	6.07e+01	7.31e+01	7.31e+01	7.31e+01	7.31e+01	8.79e+01										
		Applicatio	Applicatio	Applicatio	, Applicati	Applicatio	, Applicati	Applicatio	, Applicati	, Applicati	Applicatio	, Applicati	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	, Applicati						
	Description	Sequence 4,	Sequence 3,	Sequence 6,	Sequence 10	Sequence 8,	Sequence 4,	Sequence 2,	Sequence 2,	Sequence 4,	Sequence 2,	Sequence 4,	Sequence 14	Sequence 4,	Sequence 14	Sequence 14	4	14	Sequence 2,	Sequence 25				
	Ð	PCT-US95-1	PCT-US91-0	PCT-US96-1	US-08-469-	US-08-792-	US-07-949-	US-08-115-	PCT-US93-0	US-08-017-	US-07-941-	US-08-115-	US-07-745-	US-07-941-	US-08-165-	US-07-921-	PCT-US93-0	PCT-US94-1	PCT-US94-0	US-08-446-	US-08-220-	US-08-445-	OS-01-670-	us-01-116-
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	Length DB	716	10	176	2509	199	199	199	199	199	199	296	296	296	296	296	296	296	1271	829	829	829	829	26
æ	Query	34.7	33.7	31.6	31.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.1	30.1	30.1	30.1	29.6
	Score	89	99	62	62	9	9	9	9	9		9	9	9	9	9	9	9	9	59	59	. 59	59	28
	Result No.		7	٣	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

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                                                                                                                  OPERATIONS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REFERENCE/DOCKET NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
TYPE: ATRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 60; DB 1; Length 199;
Pred. No. 6.07e+01;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/07949516A
Patent No. 5700664
GENERAL INFORMATION:
APPLICANT: Yang, Yu-Chung
APPLICANT: Bennett, Frances
TITLE OF INVENTION: A MAMMALIAN CYTOKINE, IL-11
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/949,516A
FILING DATE: 19-NOV-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: -21..0
SEQUENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/07949516A
                                                                                     E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 30.6%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
   THOUSAND OAKS
                                                                                                         COMPUTER: IBM PC COPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Protein
LOCATION: 1..178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Region LOCATION: -21..0
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                                      USA
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                                    COUNTRY: US
ZIP: 91320
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ZIP: 02140
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Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.6%; Score 62; DB 1; Lent
larity 32.0%; Pred. No. 4.17e+01;
Conservative 9; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 AA
TITLE OF INVENTION: CANCER RELATED ANTIGEN
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFWWARE: FastSEQ Version 1.5
SOFWWARE: FASTSEQ Version 1.5
SOFWWARE: FOSTSEQ VERSION 1.5
SOFWWARE: FOSTSEQ VERSION 1.5
SURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/188,426
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 08/096,908
FILING DATE: 24-JUL-1993
APPLICATION NUMBER: 07/917,716
FILING DATE: 26-JUL-1993
APPLICATION NUMBER: 07/917,716
FILING DATE: 24-JUL-1993
APPLICATION NUMBER: 34,698
REGISTRATION NUMBER: 34,698
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 052482-0113
TELEPHONE: 202-639-7700
TELEPHONE: 202-639-7700
         NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL SOURCE:
2509 AA; 273089 MW; 32011381 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2509 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 PPGLOGRIORLIQASGNHAAGILTM 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                         COUNTRY: USA
ZIP: 20004-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-792-019B-8
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Patent No. 5460810
GENERAL INFORMATION:
APPLICANT: Williams, David A.
APPLICANT: Glark, Steven C.
TITLE OF INVENTION: Depletion
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWSON and Howson
STREET: Spring House Corporate Center. D. D. D. L.
                                                                                 GENERAL INFORMATION:
APPLICANT: BENNETT, FRANCES K
APPLICANT: PAUL, STEPHAN R
APPLICANT: PAUL, STEPHAN R
APPLICANT: TANG, VU-CHUNG
TILLE OF INVENTION: A MAMMALIAN CYTOKINE, IL-11
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS - GENETICS INSTITUTE, INC.
STREET: 87 CAMBRIDGEPARK DRIVE
CITY: CAMBRIDGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 60; DB 1; Length 199;
Pred. No. 6.07e+01;
                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLILCATION NUMBER: US/08/017,522A
FILING DATE: 19930212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: GI 5174A-DIV TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 876-1210 X8574 TELEPHONE: (617) 876-5851 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
SEQUENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                      Sequence 4, Application US/08017522A
Patent No. 5371193
                            Sequence 4, Application US/08017522A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/07941372
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MEINERT, M C
REGISTRATION NUMBER: 31,544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH: 199 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.6%;
Similarity 70.0%;
7; Conservative
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Best Local Similarity
Matches 7; Conserv
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7 LQGRLQRLLQ 16
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US-07-941-372-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XXXXX
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APPLICANT: Clark, Steven C.
TITLE OF INVENTION: Method of Treating Cell Damage or
TITLE OF INVENTION: Depletion
NUMBER OF SECUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 60; DB 1; Length 199,
Pred. No. 6.07e+01;
....matches 0; Indels
                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/941,372
FILING DATE: 19920902
CLASSIFICATION: 424
ATTONNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REGISTRATION NUMBER: 31,215
REGISTRATION NUMBER: 1NDUS1
TELEPHONE: (215) 540-9206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spring House Corporate Cntr, P.O. Box 457
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APPLICATION NUMBER: US/08/115,680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
JENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08115680 Patent No. 5437863 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08115680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 119477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 199 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Spring House
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
                                     Pennsylvania
Spring House
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                                                                          USA
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                                                                                                        19477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 11
US-08-115-680-4
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                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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02-SEP-1992

FILING DATE:

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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 19920728
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 07/652,531
FILING DATE: 06-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 07/745,382
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: CSGTT, LUADN
REFERENCE/POCKET NUMBER: 91,822
REFERENCE/POCKET NUMBER: 915188A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 60; DB 1; L
Pred. No. 6.07e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 296 AA; 31769 MW; 414378 CN;
                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: Thu Jul 30 09:13:14 1998 Job time: 6 secs.
                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617) 876-11.
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 296 amino acids
AMINO ACID
                                                               Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 30.6%;
Best Local Similarity 70.0%;
Matches 7; Conservative
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               STREET: 8/ Commontage
                                                                                       U.S.A.
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                                                                                     COUNTRY: U ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                              PEPTIDE AND PROTEIN FUSIONS TO THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED THIOREDOXIN-LIKE MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/07921848
Patent No. 5292646
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: Lavallie, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioredoxin and Thioredoxin-Like Molecules
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                           STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
21P: 02140
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentl NELease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,301A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 296;
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Pred. No. 6.07e+01;
                                                                                                                                           APPLICANT: MCCOY, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Rathleen
APPLICANT: Grant, Rathleen
APPLICANT: LaVallie, Edward R.
TITLE OF INVENTION: THIOREDOXIN, THIORE
ITILE OF INVENTION: THIOREDOXIN-LIKE MONDABER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                       E: Genetics Institute, Inc.
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI 5188D
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SEQUENCE 296 AA; 31769 MW; 414378 CN;
                                                                                     Application US/08165301A
                                           Sequence 14, Application US/08165301A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/07921848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MALDENT, M. C.
REGISTRATION NUMBER: 33.544
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPRONE: (617) 876-1170
TELERAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 296 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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Similarity 70.0%;
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                      Patent No. 5646016
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 LQARLDRLLR 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
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US-07-921-848-14
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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Length 296; 0; Indels

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:08:48 1998; MasPar time 5.39 Seconds 257.683 Million cell updates/sec :uo un

ular output not generated. Title:

>US-08-938-548A-3 (1-33) from US08938548A.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL.33 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

140542 segs, 42109429 residues

Searched:

Database:

sptrembl5
1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 30.295; Variance 46.908; scale 0.646

Statistics:

## SUMMARIES

Result No.	Score	Query	Query Match Length DB	DB	ΙD	Description	Pred. No.
+	77	30.1	363	4	002839	PORCINE MEMBRANE COFAC	5.22e-02
7	74	28.9	750	ო	093473	F14B4.1 (FRAGMENT).	1.77e-01
m	73	28.5	683	m	022187	T05A1.3.	2.65e-01
4	73	28.5	1876	m	024453	PHOSPHOINOSITIDE 3-KIN	2.65e-01
ស	73	28.5		m	001938	PHOSPHOINOSITIDE 3-KIN	2.65e-01
9	73	28.5		m	024209	PHOSPHOINOSITIDE 3-KIN	2.65e-01
7	72	28.1	147	10	061639	3' ORF.	3.94e-01
œ	72	28.1	815	σ	033367	DNA GYRASE B SUBUNIT.	3.94e-01
0	70	27.3	426	m	001969	SIMILAR TO GALACTOKINA	8.65e-01
10	70	27.3		12	091493	DYSTROPHIN (FRAGMENT).	8.65e-01
11	68	26.6	641	σ	048791	TET.	1.87e+00
12	68	26.6			048712	TETRACYCLINE RESISTANC	1.87e+00
13	68	26.6	1382	77	090975	TYROSINE KINASE.	1.87e+00
14	99	25.8	479	σ	P94426	HOMOLOGUE OF REGULATOR	3.99e+00
15	65	25.4	197	7	028584	KAP5.5 KERATIN PROTEIN	5.80e+00
16	65	25.4	589	H	013388	BETA-D-FRUCTOFURANOSID	5.80e+00
17	64	25.0	310	m	001473	COSMID CO4E6.	8.38e+00
18	64	25.0	369	σ	P75863	FROM BASES 996879 TO 1	8.38e+00
19	64	25.0	397	δ	044258	1-CARBOXY-3-CHLORO-3,4	8.38e+00
20	64	25.0	398	m	018373	SELD PROTEIN.	8.38e+00

8.38e+00	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	2.47e+01	2.47e+01
SELENOPHOSPHATE SYNTHE	REPRESSOR/INDUCER PROT	COSMID C27A2.	RIBONUCLEASE.	T21B10.6.	F21C3.1.	AMINO ACID TRANSPORTER	TETRACYCLINE RESISTANC	TETRACYLINE RESISTANCE	ORF11.	TETM GENE.	LET 858.	SIMILARITY TO EGF-LIKE	NONMUSCLE MYOSIN HEAVY	NONMUSCLE MYOSIN HEAVY	NONMUSCLE MYOSIN HEAVY	DNA FOR DNAJ, COMPLETE	NONMUSCLE MYOSIN HEAVY	NONMUSCLE MYOSIN HEAVY	T24D5.1.	N-METHYL-D-ASPARTATE R	N-METHYL-D-ASPARTATE R	N-METHYL-D-ASPARTATE R	TRKB (FRAGMENT).	MYOSIN HEAVY CHAIN, NO
018597	002606	Q18238	004393	022627	019671	039135	053770	602790	057224	047810	017336	018857	027991	012989	05120	033700	962707	062706	922732	012879	063728	008948	091373	002015
m	σ	m	œ	m	ო	œ	σ	1	σ	σ	m	m	4	N	4	σ	2	2	m	7	10	9	12	12
398	146	188	227	366	405	466	639	639	639	639	897	2946	66	106	109	157	272	282	304	1464	1464	1464	282	2007
25.0	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	23.8	23.8
64	63	63	63	63	63	63	63	63	63	63	63	63	62	62	62	62	. 62	62	62	62	62	62	61	61
21	22	23	24	25	56	27	28	58	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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MEDLINE; 94150718.
MEDLINE; 94150718.
MEDLINE; 94150718.
MILSON R., AINDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURRON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAM J., KIRSTEN J., LAISTEN N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCHURRAY A., MORTIMORE B., O'CALLAGRAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WAITERTON J.,
WATOR 368:32-38(1994).
                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).
EUKRRYOTA: METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
CHONDRICHTHYES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 70; DB 3; Length 426; Pred. No. 8.65e-01; 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATTUNG S., GELA D., WILSON R.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL. AF003739; G2105488; --
PROSITE; PS00627; GHMP KINASES_ATP; 1.
SEQUENCE 426 A3; 47290 MW; 7CBEF743 CRC32;
                                                                                                                                                            LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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EMBL; M37645; G397971; -.
NON_TER PROSITE; PS01159; WW_DOMAIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 92064638.
YEADON J.E., LIN H., DYER S.M., BURDEN S.J.;
J. CELL BIOL. 115:1069-1076(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   883 AA
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05, LAST ANNO
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                                                                                                                                       CREATED)
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5 DC-CROKTCSCRLYELLHGA-GNHAAG 29
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                                                                                    PRT;
                                                                                                                                                            (TREMBLREL. 04, (TREMBLREL. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 48.1%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                  PRELIMINARY;
                                                                                                                                    01-JUL-1997 (TREMBLREL. 04,
                                                                                                                                                                                                              SIMILAR TO GALACTOKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                   ELEGANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 92064638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WATERSTON R.;
                                                                                                                                                            01-JUL-1997
01-JAN-1998
                                                                                                                                                                                                                                            M01D7.4.
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091493
091493;
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ID 001969
AC 001969;
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PATTAN Y., BOULTON N., RON E., ROSENBERG E., ORR E.;
SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING
OF DOUBLE-STRANDED DNA.
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C5/B1/6;
MEDLINE; 92249159.
POIRIER F., CHAN C.T.J., TIMMONS P., ROBERTSON E.J., EVANS M.J.,
RIGBY P.W.J.; EVANS TI3:1105-1114(1991).
EVBL.CPMENT 113:1105-1114(1991).
EMBL; X58196; G51133; -..
SEQUENCE 147 AA; 16309 MW; 6DC857F5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
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                                                                                                                               Score 73; DB 3; Length 1876; Pred. No. 2.65e-01; 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.1%; Score 72; DB 10; Length 147; Similarity 32.1%; Pred. No. 3.94e-01; 9; Conservative 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 72; DB 9; Length 815;
Pred. No. 3.94e-01;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; MYXOBACTERALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                               DF107ECF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ000543; E1168188; -.
PROSITE; PS00177; TOPOISOMERASE_II; 1.
ISOMERASE; TOPOISOMERASE; ATP-BINDING.
SEQUENCE 815 AA; 89636 WW; 65A25520 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                             147 AA
J. BIOL. CHEM. 271:13892-13899(1996).
EMBL: U52192; G1272420; -
FLYBASE: FBGNO015278; P13K6BD.
SEQUENCE 1876 AA; 210505 MW; DFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 CCRQKTCSCRLYELLHGAGNHAAGILTL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 CCNONHYTTCLRNLLQGEAERTDGVNIL 93
                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                      501 RRKTCT-RLYELISDQRTDDPELL 523
                                                                                                                                                                                                                                                                   691 PSCRRRSTWSCRLCAEHLRGAG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 PDCCROKTCSCRLY-ELLHGAG 24
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1,1
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                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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59.1%;
                                                                                                                               Query Match 28.5%;
Best Local Similarity 41.7%;
Matches 10; Conservative
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01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
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RESULT

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SUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
SUTHERIA; ARTIODACIYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 65; DB 4; Length 197;
Pred. No. 5.80e+00;
2; Mismatches 3; Indels
                                                                                                                       Score 66; DB 9; Length 479;
Pred. No. 3.99e+00;
5; Mismatches 5; Indels
                OGASAWARA N., YOSHIKAWA H., DANCHIN A.; (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
KRAPS. 5. KERATIN PROTEIN (FRAGMENT).
                               SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA EMBL; D50453; G1805458; --
EMBL; Z99106; E1182356; --
SEQUENCE 479 Aa; 55166 MW; 3C2DIF5A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1
197 AA; 17474 MW; 731C19CA CRC32;
                                                                                                                                                                                                                                                                                                        197 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JENKINS B.J., POWELL B.C.;
J. INVEST. DERMATOL. 103:310-317(1994).
ERBL: X73435; G313722; -.
                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                       Query Match
Best Local Similarity 41.2%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.4%;
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                             207 RMYQLLKNAGKQVKTIM 223
                                                                                                                                                                                                                   |:|:|| ||:: |:
15 RLYELLHGAGNHAAGIL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
FISSUE-WOOL FOLLICLE;
MEDLINE; 94358466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                   RESULT 15
ID Q28584
AC Q28584;
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Search completed: Thu Jul 30 09:09:09 1998 time: 21 secs.

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3 LPDCCRQKTCSC 14

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Release 3.1A John F. Collins, Blocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:08:19 1998; MasPar time 3.18 Seconds 260.375 Million cell updates/sec Run on:

ular output not generated.

>US-08-938-548A-3 (1-33) from USO8938548A.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

69111 seqs, 25083644 residues Searched:

Post-processing: Minimum Match 08 Listing first 45 summaries

Database:

Statistics:

swiss-prot35 1:swiss1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 31.693; Variance 44.992; scale 0.704

### SUMMARIES

	•	_	_	_	_		_	_	_	_	_	_	_	_	_	_	_	_	_	_	_	_	_
Pred. No.	5.12e-02	1.20e-01	2.76e-01	4.17e-0]	6.26e-01	6.26e-01	1.40e+00	1.40e+00	2.07e+00	2.07e+00	2.07e+00	2.07e+00	3.06e+00	3.06e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	6.60e+00	6.60e+00
Description	CASPASE-11 PRECURSOR (	PUTATIVE TRANSMEMBRANE	PUTATIVE ACID PHOSPHAT	60S RIBOSOMAL PROTEIN	SPERM MITOCHONDRIAL CA	PUTATIVE FORKHEAD-RELA	IG ALPHA CHAIN C REGIO	MEIOTIC RECOMBINATION	UDP-GLUCOSE 4-EPIMERAS	UDP-GLUCOSE 4-EPIMERAS	PHOSPHORIBOSYLAMINOIMI	INTERFERON-ACTIVATABLE	HYPOTHETICAL PROTEIN M	MITOCHONDRIAL INHERITA	OMEGA-AGATOXIN IIIA.	OMEGA-AGATOXIN IVB PRE	BOLA PROTEIN HOMOLOG.	AGOUTI SWITCH PROTEIN	AGOUTI SWITCH PROTEIN	AGOUTI SWITCH PROTEIN	VACUOLAR PROCESSING EN	PROTEIN ECSC.	ANGIOTENSINOGEN PRECUR
А	ICEB_MOUSE	NMA_HUMAN	PPAW_CAEEL	R10A_TRYBR	MCS_MOUSE	YUL2_CAEEL	ALC_RABIT	RE11_SCHPO	GALE_RAT	GALE_HUMAN	PURK_PSEAE	IFIS_MOUSE	Y115_METJA	MD12_SCHPO	TX03_AGEAP	TX4B_AGEAP	BOLA_HAEIN	AGSW_VULVU	AGSW_MOUSE	AGSW_HUMAN	VPE_VICSA	ECSC_BACSU	ANGT_MOUSE
BB	Н	-	ч	Н	Н	Н	Н	-	Н	н	Н	Н	н	Н	Н	~	Н	Н	H	H	Н	Н	1
Length	373	260	450	214	197	461	299	923	347	348	360	425	155	273	16	83	103	125	131	132	493	236	477
Query Match	29.3	28.5	27.7	27.3	27.0	27.0	26.2	26.2	25.8	25.8	25.8	25.8	25.4	25.4	25.0	25.0	25.0	25.0	25.0	25.0	25.0	24.6	24.6
Score	. 75	73	7.1	70	69	69	67	49	99	99	99	99	65	65	64	64	64	64	64	64	64	63	63
Result No.	7	7	m	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

29.3%; Score 75; DB 1; Length 373;

Query Match

6.60e+00	9.61e+00	9.61e+00	9.61e+00	9.61e+00	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01
TETRACYCLINE RESISTANC	GLUTAMATE (NMDA) RECEP	(NMDA)	SPA2 PROTEIN.	MYOSIN HEAVY CHAIN, NO	GENE 34 PROTEIN.	UREASE OPERON URED PRO	UREASE OPERON URED PRO	HYPOTHETICAL PROTEIN K	TUBULIN BETA CHAIN.	PRPD PROTEIN.	GLYCINE BETAINE TRANSP	DNA REPAIR PROTEIN RAD	HYPOTHETICAL 37.9 KD P	MITOGEN-ACTIVATED PROT	HYPOTHETICAL 51.7 KD P	TETRACYCLINE RESISTANC	HYPOTHETICAL 118.6 KD	DNA POLYMERASE (EC 2.7	HYPOTHETICAL 133.0 KD	THYROGLOBULIN PRECURSO
TET9_ENTFA	NME1 RAT	NME1 MOUSE	SPA2_YEAST	MY SO_HUMAN	VG34_HSVEB	URED_KLEAE	URED_KLEPN	Y129_HUMAN	TBB_TRYBR	PRPD_SALTY	BETP_CORGL	RAD5_YEAST	YHO5_YEAST	NTF6_TOBAC	YMT1_CAEEL	TETM_UREUR	YAF3_SCHPO	DPOL_ADE07	YIC6_YEAST	THYG BOVIN
	4		Н	Н	Н	Н	Н	-	Н	Н	н	н	Н	н	Н	Н	-1	Н	~	Н
639	1464	1464	1466	1976	160	270	270	406	442	483	595	1169	334	371	471	639	1039	1122	1150	2769
24.6	24.2	24.2	24.2	24.2	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4
63	62	62	62	62	61	61	61	61	61	61	19	61	9	9	9	09	09	09	9	09
24 25	<b>5</b> 2	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

STANDARD; PRT; 373 AA. ; EL. 35, CREATED) REL. 35, LAST SEQUENCE UPDATE) REL. 35, LAST ANNOTATION UPDATE) OR CASPL.	MUS MUSCULUS (MOUSE). EUTRARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA. [1] SEQUENCE FROM N.A. SERAIN-CSTALL/G X CBA; TISSUE-THYMUS; MEDLINE; 96355393. WANG S., MIURA M., JUNG Y.K., ZHU H., GAGLIARDINI V., SHI L., GREENBERG G.M. H., YDAN J.;	12] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM M.A. SEQUENCE FROM N.A. SEARIN-CAPILAN; WEDLINE; 97190206. VAN DE CRAEN M., VANDENABEELE P., DECLERCO W., VAN DEN BRANDE I., FYENS M.; FYERS W.;	61-69(1997). NOVINDED IN THE PAINTED IN T	22; CASPASE_CYS; 1.  10 PROTEASE; APOPTOSIS; ZYMOGEN.  17 POTENTIAL.  18 CASPASE-11 SUBUNIT P20.  17 285 POTENTIAL.  18 373 CASPASE-11 SUBUNIT P10.  19 256 BY SIMILARITY.  14 254 BY SIMILARITY.  152 K-> N (IN REF. 2).  153 K-> N (IN REF. 2).
AR SP	E). CHORI TIS TUNG N JUNG N	ANDENAE	69(1997) ILVED IN R APOPT CODIMER LIONGS 1 5318; 5318; 5510; ASPL. CASPASE	CASPASI ROTEASI 266 285 373 373 152 42756
8735; 7 (RE 7 (RE 7 (RE PREC PREC	LUS (MOUSE); METAZOA; RODENTIA. FROM N.A. 7BL/6 X CE 96355393. MIURA M.,	CHEM. 2/1 FROM N.A. H/AN; 97190206. PAEN M., V	ETT. 403:61- NCTION: INVO SPONSIBLE FO BUNIT: HETER MILARITY: BE SPASE FAMILY US9463; G157 Y13089; E315 Y13089; E315 X13089; E315 X13089; E315 X13089; E315	S01122; THIOL F 1 80 267 286 206 254 152 373 AA;
LT 1 ICEB_MOUSE P70343; 008 01-NOV-1997 01-NOV-1997 CASPASE-11 CASPAI OR I	HERIA; HERIA; HERIA; HERIA; UENCE MINE; KAIN-C5	J. BIOL. CHEM. S. COUENCE FROM N STRAIN-C3H/AN; MEDLINE; 971902, VAN LOO G., MOLI	FEBS LETT. 403:	PROSITE; P HYDROLASE; PROPEP CHAIN PROPEP CHAIN ACT_SITE ACT_SITE CONFLICT SEQUENCE
RESULT ID AC AC DT O DT O DE CC	0000 8	R R R R R R R R R R	7000000	XXIIIIIII S

Gaps

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THIS IMMUNOGLOBULIN BELONGS TO THE IGA-G SUBCLASS. IT WAS ISOLATED FROM A RABBIT HOMOZYGOUS FOR A2, N80, DE12,15, F71, G75 HEAVY
                       NUCLEIC ACIDS RES. 12:1657-1670(1984).
-!- FUNCTION: IG ALPHA IS THE MAJON IMMUNOGLOBULIN CLASS IN BODY SECRETIONS. IT MAY SERVE BOTH TO DEFEND AGAINST LOCAL INFECTION AND TO PREVENT ACCESS OF FOREIGN ANTIGENS TO THE GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-SKELETAL MUSCLE;
MEDLINE; 90184840.
ZESCHNIGK M., WILCKEN-BERGMANN B., STARZINSKI-POWITZ A.;
NUCLETC ACIDS RES. 18:5289-5289(1990).
-1- FUNCTION: CATALYZES TWO DISTINCT BUT ANALOGOUS REACTIONS: THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-
  STOKLOSA C.M., SCHNEIDERMAN R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 923;
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 67; DB 1; Length 299;
Pred. No. 1.40e+00;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            923 AA; 107418 MW; B51C7725 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 67; DB 1; L Pred. No. 1.40e+00;
                                                                                                                                                                                                                                                                                                                                                                               594CED7C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
MEIOTIC RECOMBINATION PROTEIN REC11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     923 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 97231330.
LI Y.F., MUNATA M., WAHLS W.P., SMITH G.R.;
MOL. MICROBIOL. 23:866-878(1997).
EMBL; U70737; G1619901; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 CCDIMRCLCLIVNKLSEKSNQTAEILVL 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                 299 AA; 32256 MW;
                                                                                                                                                                                                                                                                            HSSP; P01857; 1PFC.
PROSITE; PS00290; IG_MHC; 2.
IMMUNOGLOBULIN C REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                26.2%;
llarity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.2%;
Local Similarity 35.7%;
Les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                              CHAIN HAPLOTYPE.
                                                                                                                             IMMUNOLOGIC SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RATIUS NORVEGICUS (RAI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|||| ::| :|
2 PLPDCCRQKTC-SC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GALACTOSE 4-EPIMERASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 PFPDCCPANSCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                       PIR; A02174; AHRB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
RE11_SCHPO
092380;
01-**
                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 9
GALE_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEIOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P18645;
                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
ID GA
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  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CREAK OCCOSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAENORHABDITIS ELEGANS.
EURARYOTA, META2OA, ACOELOMATES, NEMATODA, SECERNENTEA, RHABDITIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OKICTOLAGUS CUNICULUS (RĀBBIT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; LAGOMORPHA..
                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                        - DEVELOPMENTAL STAGE: LATE MEIOTIC AND EARLY HAPLOID CELLS.
                          SUBCELLULAR LOCATION: KERATINOUS MITOCHONDRIAL CAPSULE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 69; DB 1; Length 461;
Pred. No. 6.26e-01;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                            Score 69; bb.,
Pred. No. 6.26e-01;
......hoss 2; Indels
                                                                                                                                                                                                                          SELENIUM; SPERM; TESTIS; SPERMATOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUTATIVE FORKHEAD-RELATED TRANSCRIPTION FACTOR F26A1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SIMILARITY: CONTAINS A FORK-HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WORMPEP; F26A1.2; CE02683.
PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK_HEAD_2; 1.
HYPOTHET; PS50019; FORK_HEAD_3 1.
HYPOTHETOAL PROTEIN; DNA BINDING; NUCLEAR PROTEIN; TRANSCRIPTION REGULATION.
                                                                                                                                                                                                                                                  SELENIUM.
SELENIUM.
SELENIUM.
W; 4E56990C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 FORK-HEAD.
54171 MW; FB2C37B7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
03 ALPHA CHAIN C REGION (FRAGMENT).
0RYCTOLAGUS CUNICULUS (RABBIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    461 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 AA
STRUCTURE OF THE SPERM MITOCHONDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                      34 S
21015 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.0%;
Llarity 35.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 71.**,
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                               27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 RHVLCKCQLFDVLQVEG 237
                                                                                                EMBL; M88463; G459886; -. EMBL; M29603; G567228; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |: | |:|::|: |
8 ROKTCSCRLYELLHGAG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 PLKPPCCPQK-CSC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 PL-PDCCRQKTCSC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U27312; G860690;
                                                                                                                                                 PIR; A37199; A37199
HSSP; P01058; 1TAB.
                                                                                                                                                                                                   MGI:96945; MCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                           197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 84144059.
                                                                                                                                                                                                                          MITOCHONDRION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 6
YUL2_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FULTON L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALC_RABIT
P01879;
                                                                                                                                                                                                                                                    BINDING
BINDING
BINDING
SEQUENCE
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019802;

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Gaps

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DNA\_BIND SEQUENCE

셤 ö EMBL;

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                                                                                                                                                                                                             BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D., SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLATTON R.A., GGCANE J.D., KERLAYON R.A., GGCANE J.D., OVERBEER R., DOUGHERTY B.A., TOWB J.-F., ADAMS M.D., GLODEK A., OVERBEER R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A., SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., YEHRANN J.L., NGUYEN D., UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C., COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M., SCIENCE 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                               ARCHAEBACTERIA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 65; DB 1; Length 273; Pred. No. 3.06e+00; 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 65; DB 1; Length 155;
Pred. No. 3.06e+00;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BERGER K.H., SOGO L.F., YAFFE M.P.;
SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: TO YEAST MDM12.
EMBL, UG4674; G1655884; --
MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDM12.
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL PROTEIN.
SEOUENCE 155 Aa; 17727 MW; 9D9D61E8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 AA; 30517 MW; 9024B3CC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MD12_SCHPO STANDARD; PRT; 273 AA. 092377; C1-NOV-1997 (REL. 35, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) MITOCHONDRIAL INHERITANCE COMPONENT MDM12.
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01-0CT-1993 (REL. 27, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
                                           01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROTEIN MJ0115.
                    155 AA
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                     PRT;
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 53.3%;
Matches 8; Conservative
                    STANDARD;
                                                                                                                                METHANOCOCCUS JANNASCHII
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19 LLHGAGNHAAGIL 31
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01-FEB-1994 (REL. 28
OMEGA-AGATOXIN IIIA.
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Q57579:
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P33034;
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                                                                     TISSUE-VENOM;
MEDLINE; 92129351.
VENEMA V.J., SAIDEREK K.M., LEE T.D., HATHAWAY G.M., ADAMS M.E.;
VENEMA V.J., SAIDEREK K.M., LEE T.D., HATHAWAY G.M., ADAMS M.E.;
J. BIOL. CHEN. 267:2610-2615(1992).
J. BIOL. CHEN. 267:2610-2615(1992).
CALCIUM CHANNELS. THEY BLOCK INSECT NEUROMUSCULAR TRANSMISSION PRESYNAPTICALLY. POTENT BLOCKER OF N. AND L-TYPE CALCIUM CHANNELS.
J.P. PTH. SIX DISULFIDE BONDS ARE PRESENT (PROBABLE).
PIR; A42335, A42335.
VENOM: NEUROTOXIN; CALCIUM CHANNEL INHIBITOR; PRESYNAPTIC NEUROTOXIN.
SEQUENCE 76 AA; 8518 MW; C7EAOE12 CRC32;
                                                                                                                                                                                                                                                                                                                                                  Gaps
AGELENOPSIS APERTA (FUNNEL-WEB SPIDER).
EUKARYOTA; METAZOA; ARTHROPODA; CHELICERATA; ARACHNIDA; ARANEAE.
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                                                                                                                                                                                                                                                                                                          Length 76;
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Pred. No. 4.51e+00;
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Best Local Similarity 38.1%;
Matches 8; Conservative
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Search completed: Thu Jul 30 09:08:29 1998 Job time: 10 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:07:26 1998; MasPar time 4.27 Seconds 282.006 Million cell updates/sec ular output not generated. Run on:

>US-08-938-548A-3 (1-33) from USO8938548A.pep 256

1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

120441 seqs, 36531193 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

p1r56 Database:

Mean 30.310; Variance 51.743; scale 0.586 Statistics:

1:pirl 2:pir2 3:pir3 4:pir4 5:nrl3d

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Pred. No.	9.01e-01	1.84e+00	2.63e+00	2.63e+00	3.73e+00	5.28e+00	5.28e+00	7.44e+00	7.44e+00	7.44e+00	1.05e+01	1.05e+01	1.05e+01	1.46e + 01	1.46e+01	1.46e+01	1.46e+01	1.46e+01	1.46e+01	1.46e+01	1.46e+01	1.46e + 01	1.46e+01
Description	hypothetical protein	dystrophin homolog -	oct2 protein isoform	sperm_mitochondrial c	tetracycline-minocycl	Ig alpha chain C regi	Ig alpha chain C regi	Д	gene D3 protein - mou	transcriptional regul	hypothetical protein	keratin KAP5.5 - shee	beta-fructofuranosida	Omega-aga-ivb (nmr, m	Omega-aga-ivb (nmr, 2	omega-agatoxin-1vb -	omega-agatoxin IVB	omega-agatoxin III, 8	omega-agatoxin IIIA -	omega-agatoxin III, 8	cell division protein	pigment deposition co	agouti protein precur
А	524303	A41130	S60079	A37199	JN0800	AHRB	S09276	S11223	156329	B69764	C64314	I46413 .	S33920	10MB	IOMA	1AGG	A44664	B54252	A42335	A54252	B64052	A46298	137143
DB	~	N	~	~	~	-	~	~	~	~	~	~	N	ហ	Ŋ	ស	Н	N	~	7	•	~	0
Length DB	147	870	93	143	641	299	338	347	425	479	155	197	589	32	48	48	48	76	92	16	103	131	132
% Query Match	28.1	27.3	27.0	27.0	26.6	26.2	26.2	25.8	25.8	25.8	25.4	25.4	25.4	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0
Score	72	70	69	69	99	67	67	99	99	99	65	65	92	64	64	64	64	64	64	64	64	64	64
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B64835 S491735 S091735 S09519 S09519 A29171 A29779 A20733 A56773 A66733 A6673 A6673 A7555 A7555 A7555 A7555 A7255 A7255 A7255 A7255 A7255 A7267 A72867 A72867 A72867 A72867 A72867 A72867 A72867 A7287	
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#### ALIGNMENTS

<b>→</b>	E hypothetical protein H19-3' - mouse NISM #formal_name Mus musculus #common_name house mouse		33		Evans, M.J.; Ridby, P.W.J.	11	T.	differentiation in vitro and at the time of implantation in	the developing embryo.	#accession S24303	##status preliminary	##molecule_type mRNA	##residues 1-147 ##label POI	##cross-references EMBL:X58196; NID:951131; PID:951133	ARY #length 147 #molecular-weight 16309 #checksum 6958	Query Match 28.18; Score 72; DB 2; Length 147;			66 CCNQNHYTTCLKNLLQGEAEKTLGGVNLL 93	6 CCROKTCSCRLYELLHGAGNHAAGILTL 33	
ENTRY	TITLE ORGANISM	DATE	ACCESSIONS	REFERENCE	1	#30	#tit			#acc	**	-	**	•	SUMMARY	Query	Matc	í	Q C	δ	

electric ray 03-Aug-1992 #sequence\_revision 03-Aug-1992 #text\_change 23-Jan-1998 A41130 A41130 #authors Yeadon, J.E.; Lin, H.; Dyer, S.M.; Burden, S.J.
#journal J. Cell Biol. (1991) 115:1069-1076
#tille Dystrophin is a component of the subsynaptic membrane.
#cross-references WIDI:92064638
#accession A41130
##molecule\_type mRNA
##residues 1-870 ##label YEA A41130 #type fragment dystrophin homolog - Pacific electric ray (fragment) 3300k subsynaptic protein from formal\_name Torpedo californica #common\_name Pacific TITLE ALTERNATE\_NAMES ORGANISM ACCESSIONS REFERENCE DATE

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RESULT

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##status
 ##residues
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#journal
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DATE
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SUMMARY
                                 GENETICS
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#superfamily immunoglobulin C region; immunoglobulin homology
immunoglobulin
                                                *superfamily immunoglobulin C region; immunoglobulin homology duplication; glycoprotein; heterotetramer; immunoglobulin;
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#title cDNA from rat cells with reconstitutive galactose-epimerase activity in E. coli.
#cross-references MID:90384816.
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stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
                                                                                                              #domain immunoglobulin homology #label IGG1\
#domain immunoglobulin homology #label IGG2\
#binding_site carbohydrate (Asn) (covalent) #status
predicted
                                                                                                                                                                                                                                                                                                                                                                                     $09276  #type fragment
Ig alpha chain c region - rabbit (fragment)
#formal_name Oryctolagus cuniculus #common_name domestic
rabbit
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UDPgalactose 4-epimerase
#formal_name Rattus norvegicus #common_name Norway rat
18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.
#journal EMBO J. (1989) 8:4041-4047
#title The 1gA heavy-chain gene family in rabbit: cloning and sequence analysis of 13 C-alpha genes.
#cross-references Mul
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#length 338 #checksum 2169
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Pred. No. 5.28e+00;
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Best Local Similarity 50.0%;
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2 PLPDCCRQKTC-SC 14
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2 PLPDCCRQKTC-SC 14
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##residues 1-3
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Alloni, G. Azevedo, V.; Bertero, M.G.; Bessleres, P.;
Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,
A.; Braun, M.; Bridnell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caddwell, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Banich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;
Guiseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood,
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#formal_name Mus sp. #common_name mouse
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
28-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tannenbaum, C.S.; Major, J.; Ohmori, Y.; Hamilton, T.A. J. Leukoc. Biol. (1993) 53:563-568
A lippolysaccharide-inducible macrophage gene (D3) is a member of an interferon-inducible gene cluster and is selectively expressed in mononuclear phagocytes.
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05-Dec-1997 #text_change
05-Dec-1997
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                                                                                                        #superfamily Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology
                                                                                                                                                                                                                       #domain UDPglucose 4-epimerase homology #label (#length 347 #molecular-weight 38225 #checksum 6947
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#length 425 #molecular-weight 47046 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                   Length 347;
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Pred. No. 7.44e+00;
10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                         2; Indels
##residues 1-347 ##label ZES
##cross-references EMBL:X53949; NID:957791; PID:957792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues 1-425 ##label RES ##cross-references GB:S62227; NID:9385702; PID:9385703
                                                                                                                                                                                                                                                                                                   Score 66; DB 2; LA Pred. No. 7.44e+00; 4; Mismatches 2.
                                                                                                                                                              galactose metabolism; isomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 PDCCRQKTCSCRLYELLHGAGNHAAGILT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #cross-references MUID:93274206
#accession I56329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.8%;
Best Local Similarity 31.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 261 CGCRIYNLGTGTG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 CSCRLYELLHGAG 24
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#authors Yu, H.; Rosen, M.K.; Schreiber, S.L.
#submission submitted to the Brookhaven Protein Data Bank, September 1993
#cross-references PDB:10MA
#domain signal sequence #status experimental #label SIG\
#product beta-fructofuranosidase #status experimental
#label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Yu, H.; Rosen, M.K.; Schreiber, S.L.
#submission submitted to the Brookhaven Protein Data Bank, September 1993
#cross-references PDB:10MB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Omega-aga-ivb (nmr, 21 structures) - funnel-weaving spider (Agelenopsis aperta) #formal_name Agelenopsis aperta
                                                                                          #binding_site carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                       predicted

#binding_site phosphate (Thr) (covalent) #status

predicted,

#binding_site phosphate (Ser) (covalent) #status

predicted

#length 589 #molecular-weight 63650 #checksum 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #checksum 7419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #length 48 #molecular-weight 5281 #checksum 7904
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                                                                                                                                                                                                                                                                                                                                                                                                                                Omega-aga-ivb (nmr, minimized average structure) funnel-weaving spider (Agelenopsis aperta) #formal_name Agelenopsis aperta
                                                                                                                                                                                                                                    Length 589,
                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
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                                                                                                                                                                                                                                  Score 65; DB 2; L
Pred. No. 1.05e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #molecular-weight 3804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.46e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 64; DB 5;
Pred. No. 1.46e+0
                                                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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#region turn (type II)\
#disulfide_bonds\
#disulfide_bonds\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #type complete
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#region turn (type
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#disulfide_bonds\
#disulfide_bonds\
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#length 35 #molecula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Resolution: not applicable Determination: NAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Resolution: not applicable Determination: NAR
                                                                                                                                                                                                                                                                                                      548 RLFDVLNG-GEQAIETLDL 565
                                                                                                                                                                                                                                                                                                                              15 RLYELLHGAGNHAAGILTL 33
                                                                                                                                                                                                                                  Query Match 25.4%;
Best Local Similarity 42.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.0%;
Best Local Similarity 45.5%;
Matches 5; Conservative
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13-16
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12-25
19-36
27-34
                                                   36,42,170,188,211,
254,259,318,322,
388,463,518,527
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#submission
                                                                                                                                                              458,475,490
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 1-23
24-589
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REFERENCE
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24-31
SUMMARY
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                                                                                                                           70,92
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Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps

Db 19 CCRGRPCRCSM 29

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Qy 6 CCRQRTCSCRL 16

Search completed: Thu Jul 30 09:08:01 1998
Job time: 35 secs.
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:09:28 1998; MasPar time 1.19 Seconds 161.980 Million cell updates/sec i ou

ular output not generated.

>US-08-938-548A-3 (1-33) from US08938548A.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

63816 seqs, 5850866 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-issued 1:5\_COMB 2:PCT9\_COMB 3:backfiles Database:

Mean 21.451; Variance 82.349; scale 0.260 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ					
Result No.	Score	Query	Length	DB	Ü	Description	Pred. No.
1	99	25.8	39	н	US-08-249-	Sequence 40, Applicati	2.23e+01
7	99	25.8	39	-	US-08-036-	40,	2.23e+01
m	99	25.8	39	7	PCT-US95-0	40,	2.23e+01
4	99	25.8	39	~	PCT-US94-0	40,	2.23e+01
ω	99	25.8	39	-	US-08-469-	40,	2.23e+01
Q	99	25.8	348	ď	PCT-US95-0	2, A	2.23e+01
7	64	25.0	1167	Н	US-08-485-	ý	3.29e+01
80	64	25.0	1168	Н	US-08-620-	6	3.29e+01
თ	62	24.2	1464	Н	DS-08-026-	'n	4.83e+01
10	61	•	42	Н	US-08-487-	Sequence 23, Applicati	5.85e+01
11	61	23.8	42	Н	US-08-480-	23,	5.85e+01
12	61	23.8	42	Н	US-08-477-	23,	5.85e+01
13	61	23.8	4	Н	US-08-137-	23,	5.85e+01
14	19	23.8		Н	US-08-233-		5.85e+01
15	9	23.4		m	5223425-6	Patent No. 5223425.	7.08e+01
16	9	23.4	334	Н	US-08-279-	Sequence 10, Applicati	7.08e+01
17	59	23.0	283	н	US-08-658-	Sequence 2, Applicatio	8.55e+01
18	59	23.0	1019	1	us-08-296-	Sequence 4, Applicatio	8.55e+01
19	59	23.0	1083	Н	US-08-296-	Sequence 2, Applicatio	8.55e+01
20	57	22.3	21	-	US-08-019-	'n	1.24e+02
21	57	22.3	48	-	US-08-379-	1,	1.24e+02
22	57	22.3	724	Н	US-08-121-	Sequence 62, Applicati	1.24e+02
23	57	22.3	724	N	PCT-US94-1	Sequence 62, Applicati	1.24e+02

1.24 e + 0.02 1.24 e + 0.02 1.24 e + 0.02 1.24 e + 0.02 1.24 e + 0.02 1.26 e + 0.02 1.50 e	n1, Mark;	
ce 2, Application (ce 20, Application (ce 8, Application 1), Application (ce 8, Application (ce 9, Application 1), Application (ce 12, Application 1), Application (ce 13, Application 2, Application 2, Application (ce 11, Application 2, Application (ce 11, Application (ce 11, Application 2, Application (ce 11, Application (ce	Paul; Michael; Marchioni,	kb storage
Sequence 2 Sequence 2 Sequence 8 Sequence 8 Sequence 9 Sequence 9 Patent No. Patent No. Patent No. Patent No. Patent No. Patent No. Sequence 1 Sequence 1 Sequence 2 Sequence 2 Sequence 2 Sequence 3 Sequence 3	PRT; 39 AA 22A 322A Stroobant, Pau Waterfield, Mi es, Ian cer, Ian on and Use	inch, 360  9,322A 55 73 73 89
US-08-363- US-08-446- US-08-357- US-08-357- US-08-097- US-08-0977- US-08-097- US-08-485- US-08-08-08- US-08-08-08- US-08-08-08- US-08-08-08- US-08-08-08- US-08-08-08- US-08-08-08-08- US-08-08-08-08-08- US-08-08-08-08-08-08-08-08-08-08-08-08-08-	11GNWE 82493 08249 08249 1811; 1811; 1811 1 Mit aratil aratil	5.25 os /08/24 94 /965,1 92 /940,3 92 92
па	STANDARD; STANDARD; Lion US/082 Lion US/08 Lion US/08 Lion US/082 Lion US/08	LE FORM: Diskette, M TEM: PC-DC rdperfect TION DATA: THE ANY-195 NN DATA: DMBER: 08, 24-MAX-195 NN DATA: UMBER: 07, 03-SEP-195 NMBER: 07, 03-SEP-195 NMBER: 07, 30-UN-195
790 11184 11184 11187 11	132A-40 STAND  10, Application US  40, Application US  516930  INFORMATION: ANT: Goodearl, AINT: ANT: Grobe, Malo OF INVENTION: EL  FOR ENVENTION: PI  FOR INVENTION:	
	ce 40, Appl. ce 40, Appl. t No. 57169; t No. 57169; FLICANT: M. PLICANT: New SEQUATE: New STATE: New STA	MEDIUM TYPE: DECEMBER RESIDABLE DECOMPUTER: DEM COPERATING SYSTER SOFTWARE: Word, RRENT APPLICATION NUM APPLICATION OF APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION NUM FILING DATE: 30 TOR APP
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                                                                                                                                                                                                                                   Length 39;
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 40, Application PC/TUS9405083C
GENERAL INFORMATION:
APPLICANT: Robert Sklar, Mark Marchionni,
APPLICANT: David I. Gwynne
TITLE OF INVENTION: MCSCLE CONDITION
NUMBER OF SEQUENCES: 185
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                 Score 66; DB 2; Le
Pred. No. 2.23e+01;
1; Mismatches 1;
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION WIMBER: 07/863,703
FILING DATE: 03-APRIL-1992
PRIOR APPLICATION DATA:
APPLICATION WIMBER: 0.K. 91 07566.3
FILING DATE: 10-APRIL-1991
ATTORNEY/AGENT INFORMATION:
NAME: HANSON, NORMAN D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 10D 5250.5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 888-3884
INFORMATION FOR SEC 1D NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
STATE: Massachusetts
ZIP: 02110-2804
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360
MEDIUM TYPE: kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SISTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05083C
FILING DATE: 06-MAY-94
                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-MAY 94
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,204
FILING DATE: 08-MAR-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059,022
FILING DATE: 06-MAY-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 40, Application PC/TUS9405083C
                                                                                                                                                                                                       TOPOLOGY: linear
ICE 39 AA; 3760 MW; 6521 CN;
                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 Query Match 25.8%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM
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PCT-US94-05083C-40
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                                                                                                                                                                                                                                                                                       6 CCRQKTCSCR 15
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Sequence 40, Application US/08469569
Patent No. 5606032
GENERAL INFORMATION:
APPLICANT: Goodearl, Andrew; Stroobant, Paul;
APPLICANT: Chen, Maio Su; Hiles, Ian
TITLE OF INVENTION: Preparation and Use
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREE: New York City
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rolf Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                          ï
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                              Length 39;
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MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 AA.
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/POCKET NUMBER: 04585/028W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPACE, (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                            Score 66; DB 2; L
Pred. No. 2.23e+01;
1; Mismatches 1
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OPERATING SYSTEM: PC-DOS
SOCTHWARE: Wordberfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,569
FILING DATE: 06-UNN-1995
CLASSIFICATION BATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: 07/865,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/865,173
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 30-UNN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,138
FILING DATE: 30-UNN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 40, Application US/08469569
                                                                                                                                                                                                                                                                             TOPOLOGY: linear
ICE 39 AA; 3760 MW; 6521 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                            Query Match 25.8%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                  TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                   8 CCR-TICACR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 CCRQKTCSCR 15
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Sequence 1, Application US/08026138E
Patent No. 5502166
GENERAL INFORMATION:
APPLICANT: MASAYOSH! MISHINA
TITLE OF INVENTION: NOVEL PROTEINS AND GENES CODING THE SAME
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nishiohata-machi
CITY: Nilgata-shi
STREET: 5214, Nishiohata-machi
CITY: Nilgata-shi
STATE: Nilgata-shi
STATE: Nilgata-shi
STATE: DAPAN
ZIP: 951
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
                                                                                                                                  Gaps
                                                                                                                                ő
                                                                                Length 1168;
                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 to 1464 (CE 1464 AA; 165489 MW; 11224000 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE TYPE: Cerebellum
PUBLICATION INFORMATION:
AUTHORS: Masayoshi MISHINA
TITLE: NOVEL PROTEINS AND GENES CODING THE SAME
                                                                                                                                                                                                                                                                                                                                             1464 AA.
                                                                             Score 64; DB 1; Le
Pred. No. 3.29e+01;
3; Mismatches 3.
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/026,138E
FILING DATE: 26-FEB-1993
APPLICATION NUMBER: UP 39563/1992
FILING DATE: 26-FEB-1992
APPLICATION NUMBER: UP 173155/1992
FILING DATE: 30-JUN-1992
APPLICATION NUMBER: UP 215017/1992
FILING DATE: 12-AUG-1992
APPLICATION NUMBER: UP 303878/1992
FILING DATE: 13-NOV-1992
APPLICATION NUMBER: UP 303878/1992
FILING DATE: 13-NOV-1992
ATORNEY AGENT INFORMATION:
NAME: Hamburg C.Buce 8
REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: 27,389
REFERENCE/DOCKET NUMBER: 27,389
RELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 986-2340
TELEFAX: (212) 953-7733
INFORMATION FOR SEQ ID NO: 1:
SUGUENCE CHARACTERISTICS:
FERENCE: 14AA amino acids
  INDIVIDUAL ISOLATE: 167p
SEQUENCE 1168 AA; 131542 MW; 7175894 CN;
                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08026138E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSTEM: MS-DOS v.5
Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1464 amino acids TYPE: amino acid STRANDEDNESS: single strand TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                          Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monse
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XX SEQUENCE 1, Applics

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CC COMPUTER EADDA

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Patent No. 5670365
GENERAL INFORMATION:
APPLICANT: Feitelson, Jerald S.
TITLE OF INVENTION: Identification of, and Uses For, Nematicidal
TITLE OF INVENTION: Bacillus thuringiensis Genes, Toxins, and Isolates
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                        Score 64; DB 1; Length 1167;
Pred. No. 3.29e+01;
3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: Florida
REFERENCE/DOCKET NUMBER: MA48DD2.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/540,104
FILING DATE: 06-CCT-1995
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAMME: SALIWANCHIK, DAVIG R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
FENCE 1167 AA; 131657 MW; 7095219 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUFTWARE: PATENTIANS SUFTWARE: CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,717A
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE, DOCKET NUMBER: MA94.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 375-800
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08620717A
                                          TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 1167 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1168 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             873 PNCCKPAACQC 883
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4 PDCCRQKTCSC 14
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US-08-620-717A-9
                                                                                                                                                                                                                                                                                          SEQUENCE
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US-08-477-383-23

RESULT

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APPLICANT: Cruz, Lourdes J.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Montooh, J. Michael
APPLICANT: Santos, Ameurfina D.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 AA.
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Pred. No. 5.85e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,800
FILING DATE: 19-CCT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-10476
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                          CITY: Washington
STATE: DC
21P: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 51, Application US/08233788A Patent No. 5535617 GENERAL INFORMATION:
APPLICANT: Dozan, James L.
                                                                                                   Sequence 23, Application US/08137800
Patent No. 5514774
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 51, Application US/08233788A
                                                                          Sequence 23, Application US/08137800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AISM: Conus ochroleucus
42 AA; 4618 MW; 9505 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-302
INFORMATION FOR SEQ ID NO: 23
SEQUENCE CHARACTERISTICS:
FUNCTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PLP-DCCROKTCSCRLYEL 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE
ORGANISM: COI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JT 14
US-08-233-788A-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
              XXXXXX
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                                                                                                                                                                                                              APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hallyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,383

FILING DATE: 10-0CT-1995

REPLICATION NUMBER: US 08/137,800

FILING DATE: 19-0CT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/084,848

FILING DATE: 29-JUN-1993

ATORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

RESTSENDING/DOCKET NUMBER: 24260-107673

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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                                           42 AA
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5.85e+01;
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                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 61; I
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                               Sequence 23, Application US/08477383
Patent No. 5589340
GENERAL INFORMATION:
                                                                                                                                      Sequence 23, Application US/08477383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NÔ
ORIGINAL SOURCE:
ORGANISM: Conus ochroleucus
UENCE 42 AA; 4618 MW; 9505 CN;
                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 23.8%;
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 PVPSDCCQVSSCW-NLYGL 31
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Gaps

TYPE: amino acid STRANDEDNESS:

SEQUENCE

RESULT 13 ID US-08-137-800-23

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:06:53 1998; MasPar time 3.32 Seconds 152.287 Million cell updates/sec ular output not generated. .. 0

(1-33) from US08938548A.pep Title:

256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

124785 seqs, 15338987 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part13 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Mean 22.991; Variance 84.736; scale 0.271 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Length DB ID Description Pred. No. 373 18 R98461 Murine Intercent in 6.26e+00 373 18 R65767 Murine Intercent in 6.26e+00 373 18 R65767 Murine intercent in 9.46e+00 10.2 1 P95679 Kenopus Vg1 protein f 5.80e+01 848 20 W01619 Kenopus Vg1 protein f 5.80e+01 848 20 W01619 Kenopus Vg1 protein f 5.80e+01 85 20 W01619 Kenopus Vg1 protein f 5.80e+01 85 23 W10106 Human agouti signall 8.59e+01 86 23 W10105 AGI toxin. An agouti signall 8.59e+01 86 23 W10105 AGI toxin. An adouti signall 8.59e+01 8 844209 Kenopus Calcum Channel inhib 8.59e+01 8 W10101 Murine agouti signall 8.59e+01 8 W10101 Murine agouti signall 8.59e+01 130 23 W10101 Murine agouti signall 8.59e+01 1167 27 W1053 Bacillus thuringiensi 8.59e+01 1167 27 W1053 Bacillus thuringiensi 8.59e+01 1167 20 W10653 Bacillus thuringiensi 8.59e+01 1168 20 W10653 Human NWDA R2A recept 1.27e+02 1464 10 R55529 Human NWDA R2A recept 1.27e+02			æ					
23 W12414 Porcine complement in 18 R98461 Murine ICE-ced-3 homo 13 R66767 Murine interleukin-1 6 P95679 Murine interleukin-1 195679 Eysphosphatidic acid 20 W01619 Human uridine diphosp 5 P20020 Sequence of a foot an 8 W10105 Murine agouti signall AG1 toxin.  13 W10105 Murine agouti signall AG1 toxin.  14 R60293 Calcium channel inhib R44209 A. aperta venom fract 2 W10102 Human agouti signall 27 W31504 Bacillus thuringiensi NG103 Bacillus thuringiensi NG1368 Pacillus thuringiensi 10 R55629 Human NWDA R2A recept	Query Score Match Le			ngth	DB	a	Description	
18 R98461 Murine ICE-ced-3 homo 3 R66767 Murine interleukin-1 2 Murine interleukin-1 2 Murine interleukin-1 3 F05767 Lysophosphatidic acid 1 P95679 Xenopus Vgl protein f 5 W01619 Human uridine diphosp 5 P20020 Sequence of a foot an 7 Mullo Human agouti signall 8 R4010 Murine agouti signall 8 R44209 A. aperta venom fract 8 Mullo Human agouti signall 8 R44209 Human agouti signall 8 Mullo Human agouti signall 8 W1010 Human agouti signall 8 W1010 Human agouti signall 8 W1010 Human agouti signall 8 Murine agouti signall 8 Murine agouti signall 8 Mullos Human agouti signall 8 Murine Agouti Signal 8 Murine	77 30.1	30.1		363	23	W12414	Porcine complement in	6.26e+00
13 R66767 Murine interleukin-1 5 W29877 Lysophosphatidic acid 3 Lysophosphatidic acid 3 Lysophosphatidic acid 3 W01619 Ruman uridine diphosp 5 P20020 Sequence of a foot an 7 W0100 Human agoutt signall 8 W4561 AG1 toxin.  1 R6053 AG1 toxin.  1 R6053 AG1 toxin.  2 W10102 Human agoutt signall 8 W10102 Human agoutt signall 8 W10102 AG1 toxin.  2 W10101 Murine agoutt signall 8 W10101 Murine agoutt signall 8 W10101 Human agoutt signall 8 W10101 Human agoutt signall 8 W10101 Human agoutt signall 8 W1053 Human WMD8 R2A recept 1 R55829 Human NWD8 R2A recept 1	75 29.3	29.3		373	138	R98461		9.46e+00
26 W28977 Lysophosphatidic acid 3 P95679 Xenopus Vgl protein f 5 W01619 Human auridine diphosp 5 P20020 Sequence of a foot an 7 W01010 Human agoutt signall 8 R45511 AGI toxin.  1 R6023 AGI toxin. 1 R6023 A. aperta venom fract 8 W10102 A. aperta venom fract 8 W10101 Human agoutt signall 8 W10101 Nematode toxin 1679 p 8 W10653 Bacillus thuringiensi 8 W1058 Tarantula spider veno 10 R55829 Human NWDA R2A recept 1	75 29.3	29.3		373	13	R66767	Murine interleukin-1	9.46e+00
1 P95679 Xenopus Vq1 protein f 5 W01619 Human uridine diphosp 5 P20020 Sequence of a foot a f	69 27.0	27.0		329	56	W29877	Lysophosphatidic acid	3.20e+01
20 W01619	66 25.8	25.8		102	٦	P95679	Xenopus Vql protein f	5.80e+01
2 P20020 Sequence of a fot an 7 Munan agoutt signall 8 M4501 Murine agoutt signall 8 M45023 Calcium channel inhib 8 M44209 A. aperta venom fract 8 W10101 Human agoutt signall 8 M4101 Human agoutt signall 8 M31504 Bacillus thuringiensi 8 M1053 M31504 Bacillus thuringiensi 8 M1053 M31504 Bacillus thuringiensi 8 M1053 M31504 Bacillus thuringiensi 10 M5588 Tarantula spider veno 10 R55829 Human NMDA R2A recept 1	66 25.8	25.8		348	2	W01619	Human uridine diphosp	5.80e+01
23 W10106 Human agouti signalli 8 W4511 AGI toxin.  11 R60293 Calcium channel inhib 8 R44209 A. aperta venom fract 8 W10102 Human agouti signalli 8 W10101 Murine agouti signalli 8 W1053 Bacillus thuringiensi 8 W16526 Human NWDA R2A recept 1 R55529 Human NWDA R2A recept 1	65 25.4	25.4		78	'n	P20020	Sequence of a foot an	7.06e+01
23 W10105 Murine agouti signall 8 R45611 AG1 toxin. 11 R60293 Calcium channel inhib 8 R44209 A. aperta venom fract 8 W10102 Human agouti signall 18 W10101 Murine agouti signall 8 W1053 Bacillus thuringiensi 8 W10653 Bacillus thuringiensi 8 W16526 Human NWDA R2A recept 10 R55529 Human NWDA R2A recept 1	64 25.0	25.0		45	33	W10106	Human agouti signalli	8.59e+01
9 R45511 AG1 toxin. 11 R60293 Calcium channel inhib 8 R44209 A. aperta venom fract 8 W10102 Human agouti signalli 8 W10101 Muxine agouti signalli 8 W10101 Nuxine agouti signalli 8 W10101 Nematode toxin 167P p 8 W10653 Bacillus thuringiensi 8 W16326 Nematocidal toxin 167 B Human Nuxin R55829 Human Nuxin R2A recept 1		25.0		45	53	W10105	Murine agouti signall	8.59e+01
11 R60293 Calcium channel inhib 8 R44209 A. aperta venom fract 8 W14209 Human agoutt signalli 8 W10101 Murine agoutt signalli 8 W10101 Murine agoutt signalli 8 W1053 Bacillus thuringiensi 8 W1053 Bacillus thuringiensi 8 W10553 Human NWDA R2A recept 10 R55529 Human NWDA R2A recept 1	•	25.0		48	σ	R45611	AG1 toxin.	8.59e+01
8 R44209 A. aperta venom fract 8 3 W10102 Human agoutt signall 1 23 W10101 Murine agoutt signall 8 27 W31504 Nematode toxin 167P p 8 20 W10653 Bacillus thuringiensi 8 W16326 Nematocidal toxin 167 B 10 R55089 Tarantula spider veno 1 10 R55529 Human NWDA R2A recept 1	64 25.0	25.0		48	Ħ	R60293		8.59e+01
23 W10102 Human agouti signalli 8 23 W10101 Murine agouti signalli 8 27 W31504 Nematcode toxin 1679 p 20 W10553 Bacillus thuringiensi 8 23 W16326 Nematcodal toxin 167 8 10 R55089 Tarantula spider veno 1 10 R55529 Human NWDA R2A recept 1	•	25.0		48	œ	R44209		8.59e+01
23 W10101 Murine agouti signall 8 27 W31504 Nematode toxin 167P p 8 20 W10653 Bacillus thuringiensi 8 21 W16126 Nematocidal toxin 167 21 R55088 Tarantula spider veno 1 21 R55529 Human NWDA R2A recept 1	25.0	_		130	53	W10102	Human agouti signalli	8.59e+01
27     W31504     Nematode toxin 167P p     8       20     W10653     Bacillus thuringlensi     8       23     W16326     Nematocidal toxin 167     8       10     R5508     Tarantula spider veno     1       10     R55529     Human NWDA R2A recept     1	25.0	_		131	23	W10101	Murine agout1 signall	8.59e+01
20 W10653 Bacillus thuringiensi 8 23 W16326 Nematcoidal Loxin 167 8 10 R5508 Tarantula spider veno 1 10 R55529 Human NWDA R2A recept 1	25.0		٦	167	27	W31504	Nematode toxin 167P p	8.59e+01
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Human N-methyl-D-aspa Human excitatory amin Glutamic acid recepto	recept	Predatory cone snail Salmonella enteritidi	Human membrane antige	,	Human bg protein asso	$\overline{}$	Cherry polyphenol oxi	DNA polyme	DNA polymerase III ho	-E2 fusion	Spider venom peptide	N-terminal sequence o	Funnel-web spider ven	Connexin-32.	Sequence of viper ven	Sequence of viper ven	Ovine FSH beta subuni	Ikaros protein.	Mouse 22B/30B (candid	Murine Lyst1 long iso
R66039 R80970 R42054	R44192 W12745	W24890 W23579	W27333 R62758	W31950	W31949	R27559	W23671	W36071	R40126	R40115	R05633	R11517	R42948	W37469	P91100	P91095	R10038	R92020	W31948	W23594
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1464 1464 1464	1464 42	59 59	253	3672	3801	140	147	334	334	367	39	44	48	283	49	49	129	334	2186	3788
24.2 24.2 24.2	24.2 23.8	23.8 23.8	23.8	23.8	23.8	23.4	23.4	23.4	23.4	23.4	23.0	23.0	23.0	23.0	22.7	22.7	22.7	22.7	22.7	22.7
625 625 637	62	61	61	61	61	9	9	9	9	9	29	29	29	29	58	28	28	28	28	28
20 21 22	23 24	25 26	27	29	30	31	32		34	32	36	37	38	39	40	41	42		44	45

## ALIGNMENTS

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DNA encoding porcine complement inhibitor - useful in porcine organ transplant to humans claim 3; Page 12-14; 20pp; Japanese.

This protein is a porcine complement inhibitor encoded by pMCPCDNA (T61098). The DNA is useful for large scale production of recombinant porcine complement inhibitor; which is useful for porcine organ transplantation into humans. The DNA clone pMCPCDNA is also useful in the analysis of the promoter region of porcine complement
                           W1244;
24-SEP-1997 (first entry)
Porcine complement inhibitor.
porcine; pig; complement; inhibitor; organ transplantation; analysis; promoter.
                                                                                                                                                                                                                                                                                                                                                                                                           09-JAN-1997.
19-JUN-1996; J01704.
20-JUN-1995; JP-178254.
(NIME-) NIPPON MEAT PACKERS INC.
(NIMA-) NIPPON HAM KK.
Murakami H, Shigehisa T, Toyomura K;
WPI; 97-087378/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           꽃
W12414 standard; Protein; 363 AA.
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ä Score 77; DB 23; Length 363; Pred. No. 6.26e+00; 7; Mismatches 9; Indels Query Match 30.1%; Best Local Similarity 39.3%; Matches 11; Conservative

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Gaps

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JT 2 R98461 standard; Protein; 373 AA.

R98461; 25-SEP-1996 (first entry) Murine ICE-ced-3 homologue, programmed cell death; mIch-2; murine ICE-ced-3 homologue; programmed cell death; RESULT ID R9 AC R9 DT 25 DE MU

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Homo sapiens.
WO9700892-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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of local endochondral bone formation in non-union fractures, inductic applicas. requiring bone formation and cartilage repair, eg in the treatment of osteoarthritis.

See also 995699995692 and N95097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human mature unidate diphosphate galactose-4-epimerase (UDP-G4E) (W01619) catalyses a reversible reaction between UDP-glucose and UDP-galactose to atlance allows galactose residues to enter into the main pathways of glucose metabolism. A deficiency of the enzyme results in galactosaemia. The amino acid sequence of UDP-G4E was deduced from a cDNA clone (T58301) derived from a human endometrial tumour library. Recombinant UDP-G4E polypeptides can be produced in transformed host (e.g. E. coli, COS, Sf9 insect) cells or expressed in vivo for use in the treatment of UDP-G4E deficiency, e.g.
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding human uridine diphosphate galactose-4-epimerase - used in the treatment and diagnosis of galactosaemia Claim 1; Page 43-44; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Human uridine diphosphate galactose-4-epimerase.
Uridine diphosphate galactose-4-epimerase; UDP-G4E; galactosaemia;
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5.80e+01; Indels
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Pred. No. 5.80e+01;
4; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                              Score 66;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 6
W01619 standard; Protein; 348 AA.
W01619;
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11-MAY-1995; W0-U05785.
(HUMA-) HUMAN GENOME SCI INC.
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Similarity 56.3%;
9; Conservative
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GB-034147.
GB-011064.
GB-025150.
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Matches 9; Conserv
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est Local Similarity
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WPI; 96-518666/51.
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WO9635778-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New agouti signal protein peptide(s) and nucleic acids - used for altering melanin prodm., for treating e.g. melasma photo-ageing spots, solar keratosis or vitiligo claim 10; Page 11; 67pp; Bagilsh.

The sequences given in W10101-29 are biologically active peptides and fragments of the agouti signalling protein (ASP) which have depigmenting activity. These peptides are useful for cosmetic purposes and for clinical application in the prevention or treatment of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human agouti signalling protein fragment #2.

Agouti signalling protein; ASP; depigmenting activity; cosmetic;
Apperpigmentary condition; melasma photoageing spots; solar keratosis;
post-inflammatory hyperpigmentation; wound healing; eumelanogenesis;
vitiligo; leucoderma; albinism; hair greying.
                                                                                                                                                                                            DNA correspo. to (part of) foot and mouth disease virus RNA - useful in prepo. of vaccines for producing antibodies against the virus Example; Fig 6: 57pp: English.

The inventors claim a DNA molecule comprising a nucleotide sequence corresp. to all or a portion of foot-and-mouth disease virus RNA (FMDV). The DNA molecule is esp. for a precursor of FMDV capsid protein. It esp. codes for FMDV protein p88 and vPl-VP4. It may code for VP4, VP2 VP3 and VP1 contiguously. The inventors also claim a vaccine for stiumlating prodn. of antibodies against FMDV in a mammal which comprises at least one of the above recombinant proteins produced by a host cell transformed with the DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hyperpigmentary conditions and diseases such as melasma photoageing spots, solar keratosis, and post-inflammatory hyperpigmentation such occurs at sites of wound healing. They can also be used to provide enhanced eumelanogenesis for treating eg. vitiligo, leucoderma, some
                                                                                                                                                                                         - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
(NATR ) National Res Dev Corp.

(WELL ) Wellcome Foundation Ltd.

Boothroyd JC. Cross GAM, Highfield PE, Winther MD, Rowlands DJ,

Brown F, Harris TJR, Lowe PA;

WPI; 82-26702E/14.
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Pred. No. 8.59e+01;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 65; DB 5; Length 78; Pred. No. 7.06e+01; 9; Mismatches 5; Indels
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21-JUN-1996; U10695.
23-JUN-1995; US-000436.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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W10105 standard; protein; 45 AA.
W10105;
17-SEP-1997 (first entry)
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W10106 standard; protein; 45 AA.
w10106;
18-SEP-1997 (first entry)
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41.2%;
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Best Local Similarity 37.5%;
Matches 9; Conservative
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Matches 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hearing VJ;
WPI; 97-087323/08.
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Hearing VJ;

WPI; 97-087323/08.

WPI; 97-087323/08.

WPI; 97-087323/08.

The altering melanin protein peptide(s) and nucleic acids - used for altering melanin prodn., for treating e.g. melasma photo-ageing spots, solar keratosis or vitiligo

Claim 5; Page 8-9; 67pp; English.

Claim 5; Page 8-9; 67pp; 67pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pacillus thuringlensis toxin gene - useful in recombinant hosts, particularly plants for the control of nematodes Claim 4; Page 35-39; 44pp. English.

Claim 4; Page 35-39; 44pp. English.

This sequence represents the protein encoded by a polynucleotide of the invention. The polynucleotide of the invention is a sequence from a Bacillus thuringlensis (Bt) isolate selected from PS80JJ, PS158D5, PS167P, PS169P, PS177FI, PS177G, PS204G4 and PS204G6, that encodes a toxin active against nematodes. This sequence represents the 167P protein, and is a delta-endotoxin protein. The polynucleotides and toxins can be used for the control of nematode pests such as Panagrellus
Agouti signalling protein; ASP; depigmenting activity; cosmetic; hyperpigmentary condition; melasma photoageing spots; solar keratosis; post-inflammatory hyperpigmentation; wound healing; eumelanogenesis; vitiligo; leucoderma; albinism; hair greying.
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Nematode toxin 167P protein.
PCR primer; amplify; nematode toxic protein; Bacillus thuringiensis; delta-endotoxin gene; nematode pest control; Panagrellus redivivus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 64; DB 23; Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Start of Cysteine-rich motif"
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                                                                                                                                                                                                                                                                                                                                                                           /note= "Start of basic region"
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/note= "Signal sequence"
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                                                                                                                                                                                                                     Location/Qualifiers
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W31504 standard; Protein; 1167
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 papaccdpcascqcrff 118
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21-MAR-1996; 004755.
21-MAR-1996; 02-590554.
(MYCO ) MYCOGEN CORP.
Fu J, Narva KE, Payne J;
WPI; 97-480163/44.
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Bacillus thuringiensis.
WO9734926-A2.
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21-JUN-1996; U10695.
23-JUN-1995; US-0004
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                                                                                                                                                                                                                                                        peptide
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The sequences given in W10101-29 are biologically active peptides and fragments of the agouti signalling protein (ASP) which have depigmenting activity. These peptides are useful for cosmetic purposes and for clinical application in the prevention or treatment of various hyperpigmentary conditions and diseases such as melasma photoageing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human agoutt signalling protein.

Agoutt signalling protein; ASP; depigmenting activity; cosmetic;

Agoutt signalling protein; ASP; depigmenting activity; cosmetic;

hyperpigmentary condition; melasma photoageing spots; solar keratosis;

post-inflammatory hyperpigmentation; wound healing; eumelanogenesis;

vitiligo; leucoderma; albinism; hair greying.
               Example; Page 17; 28pp; English.

The sequence is that of a polypeptide present in fraction K of the venom of Agelenopsis aperta, it blocks calcium channels in cells of both mammals and invertebrates, partic. those affecting neuronal and muscle cells. It may be used in the treatment of angina, hypertension, cardiomyopathies, supraventricular arrhythmia, oesophogeal achalasia, premature labour, and Raynaud's disease. It may also be of use in the study of cell physiology and in the control of invertebrate pests. It may be produced synthetically. Sequence 48 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 8.59e+01;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 64; DB 8; Length 48; Pred. No. 8.59e+01;
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86
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Murine agouti signalling protein.
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W10102 standard; protein; 130 AA
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Best Local Similarity 45.5%;
Matches 5; Conservative
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Best Local Similarity 41.28;
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21-JUN-1996; U10695.
23-JUN-1995; US-0004
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp :uo on:

Thu Jul 30 09:04:06 1998; MasPar time 9.31 Seconds 592.652 Million cell updates/sec lar output not generated.

>US-08-938-548A-2 (1-131) from USO8938548A.pep 931 1 MNLPSTKVSWAAVTLLLLLL.......GRRCSAPAASVAPGGQSGI 131 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

Searched:

140542 segs, 42109429 residues

Minimum Match 0% Listing first 45 summaries Post-processing:

sptrembl5
1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified Database:

Mean 39.725; Variance 90.808; scale 0.437 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Score	Match	Match Length	DB	1	Description	Pred. No.
н	109	11.7	602	ដ	062731	PROSTAGLANDIN H SYNTHA	2.09e-02
~	108	11.6	599	~	015122	PROSTAGLANDIN ENDOPERO	2.80e-02
m	107	11.5	602	10	063684	CYCLOOXYGENASE 1.	3.74e-02
4	107	11.5	602	30	063921	CYCLOOXYGENASE ISOFORM	3.74e-02
ហ	105	11.3	347	σ	P76559	FROM BASES 2573751 TO	6.65e-02
9	103	11.1	619	œ	023352	HYPOTHETICAL 74.6 KD P	1.18e-01
7	101	10.8	1584	~	014514	BAI 1.	2.07e-01
∞	96	10.3	205	12	042394	NISHED (FRAGMENT).	8.25e-01
σ	95	10.2	226	σ	006319	HYPOTHETICAL 23.1 KD P	1.08e+00
10	94	10.1	1337	7	015255	PROTEIN-TYROSINE PHOSP	1.42e+00
11	93	10.0	469	^	037839	ORF469 PROTEIN.	1.86e+00
12	93	10.0	1109	4	019179	GUANYLATE CYCLASE E.	1.86e+00
13	92	6.6	399	유	P97518	ANDROGEN-BINDING PROTE	2.42e+00
14	92	9.9	399	9	062588	SEX HORMONE-BINDING GL	2.42e+00
15	92	9.0	833	~	099523	SORTILIN PRECURSOR.	2.42e+00
16	90	9.7	147	9	061639	3' ORF.	4.11e+00
17	06	9.7	574	12	035298	ACYLOXYACYL HYDROLASE.	4.11e+00
18	90	7.6	066	ω	040699	LEUCINE-RICH REPEAT/RE	4.11e+00
19	83	9.6	172	2	061104	FLT3 LIGAND, T169 FORM	5.34e+00
50	83	9.6	4848	σ	007944	PRISTINAMYCIN I SYNTHA	5.34e+00

RESULT 2
AC 015122
AC 015122
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE PROSPAGIANDIN ENDOPENOXIDE SYNTHASE.
OS HOMO SAPIENS (HUMAN).
OC EUTHERIA; PRIMATES.
OC EUTHERIA; PRIMATES.
RN (1)
RN (1)
RN (1)
RA YONGWAR C., TANNEE T.;
RA HOROYAMA C., TANNEE T.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 165:888-894(1989).

6.93e+00	6.93e+00	6.93e+00	8.96e+00	8.96e+00	8.96e+00	8.96e+00	1.16e+01	1.16e+01	1.16e+01	1.16e+01	1.49e+01	1.49e+01	1.49e+01	1.49e+01	1.49e+01	1.49e+01	1.49e+01	1.49e+01	1.49e+01	1.92e+01	1.92e+01	1.92e+01	1.92e+01	1.92e+01
NOVEL SERINE PROTEASE.	PHENOLOXIDASE (EC 1.10	TIGHT JUNCTION PROTEIN	ANION EXCHANGER ISOFOR	PCBR.	ANION EXCHANGER 2 A (F	RIBOSOME RECEPTOR.	INTERLEUKIN-3.	MAV266 (FRAGMENT).	HYPOTHETICAL 30.9 KD P	VESICLE COAT PROTEIN S	LIM4 PRECURSOR (FRAGME	VRG53 PROTEIN (FRAGMEN	CTG4A.	MRNA (KIAA0081) FOR OR	LEUCINE ZIPPER WITH BA	PORCINE MEMBRANE COFAC	GLIAL GROWTH FACTOR 2	SEMAPHORIN B.	ORF 24.	1-ACYL-SN-GLYCEROL-3-P	O-POLYMERASE RFC (RFC)	LECITHIN: CHOLESTEROL A	APOER2DELTA4-7.	MC035R.
092743	013420	095168	060471	P72405	960470	028298	028334	007405	033285	002822	043535	005844	015412	014696	091640	002839	007111	062178	966627	035083	051365	035849	014968	098203
N	-1	4	10	σ	9	4	7	σ	σ	Н	ω	σ	7	7	12	4	~	10	1	10	σ	10	~	11
480	519	1174	84	551	729	1534	142	266	277	2195	100	139	143	233	331	363	422	760	767	285	438	440	793	2133
9.5	9.5	9.5	9.3	6.3	9.3	9.3	9.5	9.5	9.5	9.5	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.0	9.0	9.0	9.0	9.0
88		88	87	87	87	87	98	86	86	98	82	82	82	82	82	82	82	82	82	84	84	84	84	84
21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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RESULT

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96 FLAAADGANDASDHIQQMASACRATRLVLGGYSQGAAVIDIVTA-APLPGL-GFTQPLPP 153
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
PROTEIN TYROSINE PHOSPHATASE ETA PRECURSOR (EC 3.1.3.48) (R-PTP-ETA).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHBRAR, PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 LLSSGAAAQPLPDCCRQKTCSCRLYELLHGAGNHAAGILTLGKRRSGPPGLQGRLQRLLQ 85
                                                                                                                                                                                                                                                                       STRAIN=H37RV;
MEDLINE; 96181548.
PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN-TYROSINE PHOSPHATASE ETA. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN-TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 95; DB 9; Length 226;
Pred. No. 1.08e+00;
24; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 95086212.
HONDA H., INAZAWA J., NISHIDA J., YAZAKI Y., HIRAI H.;
BLOOD 84:4186-4194(1994).
EMBL; D3740373: -
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
SIGNAL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; HYDROLASE.
                                                DEVLIN K., CHURCHER C.M.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                         BARRELL B.G., RAJANDREAM M.A., PARKHILL J.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                    COLE S.T.;
PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996)
EMBL; 295390; E316057; -.
HYDOTHETICAL PROTEIN.
SEQUENCE 226 AA; 23113 MW; C7D17505 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIBRONECTIN TYPE-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIBRONECTIN TYPE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1337 AA.
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Local Similarity 27.3%;
hes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 AADDHIAAIALFGNPSG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                  STRAIN-H37RV;
                           STRAIN-H37RV
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CARBOHYD
CARBOHYD
CARBOHYD
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TRANSMEM
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CARBOHYD
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015255;
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
NISHED (FRAGMENT).
GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                             TIŜSUE-BRAIN;
NISHIMORI H., SHIRATSUCHI T., URANO T., KIMURA Y., KIYONO K.,
TATSUMI K., YOSHIDA S., ONO M., KUWANO M., NAKAMURA Y.;
ONCOGENE 0:0-0(1997).
EMBL; AB005297; D1024528; -..
SEQUENCE 1584 AA; 173531 MW; 235A5C42 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 101; DB 2; Length 1584;
Pred. No. 2.07e-01;
3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 KNLPGRAGL-GR-EQFLCPAARRGAGIPQLGHRASGTPRPSPALRASSCS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.3%; Score 96; DB 12; Length 205;
larity 38.0%; Pred. No. 8.25e-01;
Conservative 15; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUB-SKELETAL MUSCLE;
DHAR M., MASCARENO E., SIDDIQUI M.A.Q.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF003093; G2232184; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-JUL-1997 (TREMBLREL. 04, LAST ANNOTATION UPDATE)
HYPOTHETICAL 23.1 KD PROTEIN.
                                                                                                                                                                                                                         LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 AA; 20829 MW; 57AA0342 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 AA
                                                                                                                                                1584 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 WAAVTLILILIL-PPALLSSGAAQPLPDCC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 WILAPLILLLIGRRARAAGADAGPGPEPC 43
                                                                                                                                                                                                  CREATED)
                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.8%; (1) 10.8%; (1) 10.0%; (2) 10.0%; (3) 10.0%; (4) 10.0%; (5) 10.0%; (5) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 10.0%; (6) 
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                                                                                                                                                                                                05,
05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYCOBACTERIUM TUBERCULOSIS.
                                                                                                                                                                                           01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTCY13E12.05.
SP 656
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102 GA 103
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SEQUENCE
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006319
006319;
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셤 ò RESULTION OC DT OC DT OC DT OC DT OC DT OC OC DT OC OC DT OC DT OC OC DT OC DT

Gaps

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Gaps
                                                                                                            PETERSEN C.M., NIELSEN M.S., JACOBSEN L., TOMMERUP N., HOLM H., ROIGMAND H., GLIEMANN J., MADSEN P., MOESTRUP S.K.; SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; X98248; E246784; -
                                                                                4.
                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
30 399 SEX HORMONE-BINDING GLOBULIN.
399 AA; 43842 MW; 327FALA7 CRC32;
                                                Length 399;
                                             Score 92; DB 10; Length 399
Pred. No. 2.42e+00;
14; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 92; DB 2; Length 833;
Pred. No. 2.42e+00;
4; Mismatches 10; Indels
                                                                                                                                                                                                                               01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
SORTILIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 POTENTIAL.
833 SORTILIN.
92408 MW; D2E351B9 CRC32;
                                                                                                                                                                                                        833 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 WPHGLGLLLLLQLLPPSTLSQDRLDAPPP 42
                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 48.3%;
Matches 14; Conservative
                                           Query Match
Best Local Similarity 33.3%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      833 AA;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
 CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                      RESULT
ID 09
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Search completed: Thu Jul 30 09:04:56 1998 Job time : 50 secs.

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(MI)

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 09:03:31 1998; MasPar time 5.27 Seconds 623.327 Million cell updates/sec :uo

>US-08-938-548A-2 (1-131) from USO8938548A.pep 931 1 MNLPSTKVSWAAVTLLLLLL......GRRCSAPAAASVAPGGQSGI 131 abular output not generated.

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

69111 seqs, 25083644 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot35 1:swiss1

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 41.687; Variance 80.083; scale 0.521

#### SUMMARIES

. O		R 4.73e-03	2.43e-02	T 3.36e-02	P 6.37e-02	_	P 8.74e-02	7 1.20e-01	T 1.20e-01	P 1.64e-01	E 3.04e-01	K 3.04e-01	P 3.04e-01	N 3.04e-01	Ŋ.	IP 5.60e-01	υ.	P 5.60e-01	7.	4 1.37e+00	1.37e+00	1.37e+00	1.37e+00	Н 1.37е+00
Description		SECRETIN PRECURSOR (FR	TENSIN.	PROSTAGLANDIN G/H SYNT	PROTEIN-TYROSINE PHOSP	PROTEIN-TYROSINE PHOSP	ADENYLATE CYCLASE, TYP	URIDINE KINASE (EC 2.7	PROSTAGLANDIN G/H SYNT	HYPOTHETICAL 22.7 KD	GROWTH REGULATED PROTE	HYPOTHETICAL PROTEIN	PROTEIN-TYROSINE PHOSP	CATION-INDEPENDENT MAN	SL CYTOKINE PRECURSOR	COMPLEMENT C1Q SUBCOMP	TRANS-ACTING TRANSCRIP	TRANS-ACTING TRANSCRIP	STROMELYSIN-3 PRECURSO	SIGNAL TRANSDUCER CD24	E PROTEIN.	LYSIS PROTEIN.	SL CYTOKINE PRECURSOR	HYPOTHETICAL PROTEIN
E		SECR_PIG	TENS_CHICK	PGH1_HUMAN	PTPX_MACNE	PTPX_HUMAN	CYA6_MOUSE	URK1_MOUSE	PGH1_MOUSE	YKO7_YEAST	GRO_CRIGR	Y152_HUMAN	PTPJ_HUMAN	MPRI_BOVIN	FL3L_HUMAN	C1QB_HUMAN	ICPO_HSVBJ	ICPO_HSVBK	COGY_MOUSE	CD24_MOUSE	VGE_BPS13	VGE_BPPHX	FL3L_MOUSE	YCEC_HAEIN
ä	3	П	-	ч	Н	٦	Н	٦	Н	ч	Н	ч	Н	ч	ч	Н	Н	-	-	н	Н	Н	ч	Н
% Query Match Length		131	1744	599	1013	1015	1165	260	602	205	101	292	1337	2499	235	251	9/9	9/9	492	16	06	90	232	322
Query		11.5	11.0	10.8	10.6	10.6	10.5	10.4	10.4	10.3	10.1	10.1	10.1	10.1	6.6	6.6	6.6	6.6	8.6	9.6	9.6	9.6	9.6	9.6
9700		107	102	101	66	66	86	46	97	96	94	94	94	94	92	92	92	92	91	88	8	88	83	88
sult		П	7	m	4	ις.	ø	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

SNAKE 1.37e+00	IE-ST 1.37e+00	)R (E 1.85e+00	(EC 1.85e+00	TYP 1.85e+00	TYP 1.85e+00	JR (P 2.47e+00	EIN 2.47e+00	KD P 2.47e+00	2.47e+00	SYNT 2.47e+00	ADOT 2.47e+00	MAN 2.47e+00	BL). 3.30e+00	TED 3.30e+00	NE P 3.30e+00	LAGE 3.30e+00	: PEP 3.30e+00	YCLA 3.30e+00	E CO 3.30e+00	19.8 4.40e+00	(+) 4.40e+00
SERINE PROTEASE SN	PHOSPHATIDYLCHOLINE-ST	EPHRIN-A3 PRECURSOR	LIPASE 1 PRECURSOR	ADENYLATE CYCLASE,	ADENYLATE CYCLASE,	PROLACTIN PRECURSOR	INFECTED CELL PROTEIN	HYPOTHETICAL 36.0	HFLK PROTEIN.	PROSTAGLANDIN G/H	LUTROPIN-CHORIOGONADOT	CATION-INDEPENDENT MAN	4-1BB LIGAND (4-1BBL)	TRANSLOCON-ASSOCIATED	WNT-1 PROTO-ONCOGENE	FIBRIL-FORMING COLLAGE	ATRIAL NATRIURETIC PEP	RETINAL GUANYLYL CYCLA	MULTIDOMAIN VESICLE CO	VERY HYPOTHETICAL	GPI-LINKED NAD(P)(+)
SNAK_DROME	LCAT_MOUSE	EFA3_HUMAN	LIP1_PSYIM	CYA6_CANFA	CYA6_RAT	PRL_FELCA	ICP3_HSV1N	YCEC_ECOLI	HFLK_ECOLI	PGH1_SHEEP	LSHR PIG	MPRI_HUMAN	41BL_HUMAN	SSRA_RABIT	WNT1_MOUSE	CAFF_RIFPA	ANPA HUMAN	CYGD_HUMAN	SC16_YEAST	YCX7_YEAST	NARG_MOUSE
Н	н	Н	<del></del> 1	Н	Н	Н	-	ч	Н	Н	-	Н	Н	Н	Н	Н	٦	Н	Н	Н	П
430	438	238	317	1165	1166	229	245	319	419	9	969	2491	254	286	370	1027	1061	1103	2194	171	325
9.6	9.6	9.5	9.5	9.2	9.5	9.3	9.3	6.3	6.3	9.3	9.3	9.3	9.5	9.5	9.5	9.5	8.5	9.5	9.5	9.1	9.1
83	83	88	88	88	88	87	87	87	87	87	87	87	86	86	86	86	86	86	86	82	85
77	25	26	27	28	29	30	31	32	33	34	32	36	37	38	36	40	41	42	43	44	45

## ALIGNMENTS

RESIDENT SOLUTION OF THE PARTY
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CCCCCRAXCARRAXCARRA

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TISSUE-PANCREAS;

GLAGASSE J. M. JELINEK L., SEXSON S., LOFTON-DAY K., BREININGER J.,
SHEPPARD P., KINDSVOGEL W., HAGOPIAN W.A.;
MOL. MED. 3:163-173(1997).

-!- FUNCATION: IMPLICATED IN DEVELOPMENT OF NERVOUS SYSTEM AND
PANCREATIC ENDOCRINE CELLS.

-!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 =
PROTEIN TYROSINE + ORTHOPHOSPHATE.

-!- SUBCELLULAR LOCATION: TYRO
-!- SUBCELLULAR LOCATION: TYRO
-!- SUBCELLULAR LOCATION: TYRO
-!- TISSUE SPECIFICITY: PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTPX_HUMAN STANDARD; PRI; 1015 AA.
092932; 092662;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP-X)
(ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN)
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PROFEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP-X)
(M1851).
                                                                                                                                                                                                                                                                                                                                                                                                                 --- SIMILARITY: CONTAINS 1 PROTEIN-TERENDENT DIABETES MELLITUS.

---- SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN.

EMBL; 091574; G1916942; ---

PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.

PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.

PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.

PROSITE; PS50056; TYR_PHOSPHATASE_PTP; 1.

PROSITE; PS50056; TYR_PHOSPHATASE_PTP; 1.

PROSITE; PS50056; TYR_PHOSPHATASE_PTP; 1.

PROSITE; PS50056; TYR_PHOSPHATASE_PTP; 1.

PROSITE; PS50056; TYR_PHOSPHATASE_Y 1.

PROSITE; PS50056; TYR_PHOSPHATASE X.

SIGNAL 1013 PROTEIN-TYROSINE PHOSPHATASE X.

CHAIN 22 613 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METALOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                       MACACA NEMESTRINA (PIG-TAILED MACAQUE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 99; DB 1; Lengtu ... bred. No. 6.37e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 97032784.
KAWASAKI E., HUTTON J.C., EISENBARTH G.S.;
BIOCHEM. BIOPHYS. RES. COMMUN. 227:440-447(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111190 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 LLLLLLLPPALLSSGAAAQP 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 LLLLLLLPPRVLPAAPSSVP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.6%;
Best Local Similarity 57.1%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMITH P.D., WANG J., SUBMITTED (OCT-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1013 AA;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-PANCREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ŋ
                                                                                                        PTPRN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
        ద
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                             -: SUBCELLOLAR LOCATION: MEMBRANE-ASSOCIATED. MICROSOMAL MEMBRANE.
-: THIS ENZYME ACTS BOTH AS A DIOXYGENASE AND AS A PEROXIDASE.
-: THIS ENZYME ACTS BOTH AS A DIOXYGENASE AND AS A PEROXIDASE.
-: THIS ENZYME IS THE TARGET OF NONSTEROIDAL ANTI-INFLAMMATORY DRUGS SUCH AS ASPIRIN.
-: ALTERNATIVE PRODUCTS: TWO FORMS CAN BE PRODUCED BY ALTERNATIVE SPLICING OF THE GENE FOR THIS PROTEIN.
-: STMILARTY: CONTAINS I EGF-LIKE DOMAIN.
EMBL: S36211; G249624; -.
EMBL: S36271; G249626; -.
EMBL: S78220; G243972; -.
                                                                                                                                                                                                                                                                                                    CELLS.
-1- CATALYTIC ACTIVITY: ARACHIDONATE + AH(2) + 2 O(2) - PROSTAGLANDIN
                                                                                                                                                                                                                     DIAZ A., REGINATO A.M., JIMENEZ S.A.;
J. BIOL. CHEM. 267-110816-10822(1992).
-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN REGULATING OR PROMOTING
CELL PROLIFERATION IN SOME NORMAL AND NEOPLASTICALLY TRANSFORMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYCLOOXYGENASE (BY SIMILARITY).
PROXIMAL HEME LIGAND (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
ASPINIARITY.
ASPINIARITY.
ASPINIARITY.
SP-N: ABGLISH CYLOOXYGENASE ACTIVITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; FALSE_NEG.
OXIDOREDUCTARE; DIOXYGENASE; PEROXIDASE; GLYCOPROTEIN; ACETYLATION;
PROSTAGLANDIN BIOSYNTHESIS; HEME; IRON; SIGNAL; MEMBRANE;
EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                              TAKAHASHI Y., UEDA N., YOSHIMOTO I., YAMAMOTO S., YOKOYAMA C., MIYATA A., TANABE I., FUSE I., HATTORI A., SHIBATA A.;
BIOCHEM. BIOPHYS. RES. COMMUN. 182:433-438(1992).
                                                                                                                                                                                                                                                                                                                                        H2 + A + H(2)O.
PATHWAY: FIRST STEP IN THE FORMATION OF PROSTAGLANDINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISTAL HISTIDINE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSTAGLANDIN G/H SYNTHASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISSING (IN SHORT FORM).
8C7684CD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      %; oc...
Score 101; DB 1; Lengt
No. 3.36e-02;
No. 3.36e-7; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 LLFLLLPPLPVLLADPGAPTPVNPCC 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 LLLLLLLLP-PALLSSGAAAQPLPDCC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68656 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.8%;
Local Similarity 51.9%;
hes 14; Conservative
                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-LUNG FIBROBLAST;
MEDLINE; 92268138.
                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143
396
599 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A39937; A39937
                      SEQUENCE FROM N.A.
                                          TISSUE-PLATELET;
MEDLINE; 92134251
                                                                                                                                                                                                                                                                                                                                                                               THROMBOXANES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
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MUTAGEN
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Gaps

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Length 1013;

CYTOPLASMIC (POTENTIAL)

POTENTIAL. POTENTIAL

POTENTIAL

9EC7D263 CRC32;

SEQUENCE FROM N.A. MEDLINE; 96394649. CUI L., YU W.-P., DE AIZPURUA H.J., SCHMIDLI R.S., PALLEN C.J.; BARKER K.T., CROMPTON M.; TO EMBL/GENBANK/DDBJ DATA

PRT; 1013 AA.

STANDARD;

ILT 4 PTPX\_MACNE 002695;

RESULT ID PT AC 00

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ETT ETT S

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Gaps

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CRARARROCCSUEEDDIACO

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ANISOWICZ A., BARDWELL L., SAGER R.;
PROC. NATL. ACAD. SCI. U.S.A. 84:7188-7192(1987).
-!- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS.
-!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRICETULUS GRISEUS (CHINESE HAMSTER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                  VANDENBOL M., BOLLE P.-A., DION C., PORTETELLE D., HILGER YEAST 10:S35-S40(1994).
EMBL; 226877; G407501; -.
EMBL; Z28146; G486251; -.
                                                                                                                                                                                                                                                                                                                                                                                      Score 96; DB 1; Length 205; Pred. No. 1.64e-01; 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 PATR-SLLRAPLLLLLLLLLATSRLATGAPVANELR-CQCLQTMTGVHL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P09341; IMGS.
PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
CYTOKINE; GROWH FACTOR; INFLAMMATORY RESPONSE; SIGNAL.
SIGNAL 1
28
POTENTIAL.
                        SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EURARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRO PROTEIN.
BY SIMILARITY.
BY SIMILARITY.
'', 3F83AD41 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.1%; Score 94; DB 1; Larity 41.7%; Pred. No. 3.04e-01; Conservative 9; Mismatches 15
                                                                                                                                                                                                                                                                                                                                            22673 MW; OAEA8D4E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y152_HUMAN STANDARD; PRT; 292 AA. 014165; 01-NOV-1997 (REL. 35, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) HYPOTHERICAL PROTEIN KIAA0152. HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 LLLLLLLLLPPLPPPPSVKGEPDAC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GROWTH REGULATED PROTEIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 GR
63 BY
79 BY
10893 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQI
01-DEC-1992 (REL. 24, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C-X-C) (CHEMOKINE CXC)
EMBL; J03560; G304509; -.
PIR; B28414; B28414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                   PIR; S37804; S37804.
PIR; S44581; S44581.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 AA;
                                                                                                                                                                                                                                                                                                                                              205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
tes 20; Conser
                                                                                              SEQUENCE FROM N.A. STRAIN-S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 88041072.
                                                                                                                                              MEDLINE; 94378720
    OR YKL601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LT 10
GRO_CRIGR
P09340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
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1D Y1
AC Q1
DT Q1
DT Q1
DT Q1
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                                                      01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
PROSTAGLANDIN G/H SYNTHASE 1 PRECIRSOR (EC 1.14.99.1) (CYCLOOXYGENASE 1) (CYCLOOXYGENASE SYNTHASE 1) (PGH SYNTHASE 1) (PH SYNTHASE 1) (PGH SYNTHASE 1) (PH SYNTHASE 1) (PGH SYNTHASE 1) (PGH SYNTHASE 1) (PH SYNTHASE 1) (PH SYNTHASE 1) (PGH SYNTHASE 1) (PH SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBUNIT: HOMODIMER.
-1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MICROSOMAL MEMBRANE.
-1- THIS ENZYME ACTS BOTH AS A DIOXYGENASE AND AS A PEROXIDASE.
-1- THIS ENZYME IS THE TARGET OF NONSTEROIDAL ANTI-INFLAMMATORY DRUGS
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 90203007.
DEWITT D.L., EL-HARITH E.A., KRAEMER S.A., ANDREWS M.J., YAO E.F.,
ARMSTRONG R.L., SMITH W.L.;
J. BIOL. CHEM. 265:5192-5198(1990).
-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN REGULATING OR PRONOTING
CELL PROLIFERATION IN SOME NORMAL AND NEOPLASTICALLY TRANSFORMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: ARACHIDONATE + AH(2) + 2 O(2) - PROSTAGLANDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; FALSE_NEG.
OXIDOREDUCTASE; DIOXYGENASE; PEROXIDASE; GLYCOPROTEIN; ACETYLATION;
PROSTAGLANDIN BIOSYNTHESIS; HEME; IRON; SIGNAL; MEMBRANE;
EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISTAL HISTIDINE (BY SIMILARITY).
CYCLOOXYGENASE (BY SIMILARITY).
PROXIMAL HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REL. 29, CREATED)
(REL. 29, LAST SEQUENCE UPDATE)
(REL. 30, LAST ANNOTATION UPDATE)
L 22.7 KD PROTEIN IN SDH1-CIMS/YTA3 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H2 + A + H(2)O.
-i- PATHWAY: FIRST STEP IN THE FORMATION OF PROSTAGLANDINS AND
                                                                                                                                                                                                            MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 97; DB 1; Length 602; Pred. No. 1.20e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASPIRIN-ACETYLATED SERINE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
POTENTIALIARITY.
POTENTIAL.
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  602 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUCH AS ASPIRIN.
-1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
EMBL; M34141; G200303; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 WFPLLLLLLPPTPSVLLADPGVPSPVNPCC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGF-LIKE
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW.
                                               01-AUG-1991 (REL. 19, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.4%;
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  STANDARD;
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71
161
577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A35564; A35564.
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146
602 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THROMBOXANES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YKO7_YEAST
P36061;
01-JUN-1994
PGH1_MOUSE
P22437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
SEQUENCE
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ACT_SITE
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Gaps

4;

15;

Length 101;

DISULFID CARBOHYD

Best Loca Matches

윰 ð RESULT ID YK AC P3 DT 011 DT 011 DT DT DT DE DT DE DE DE HX

DISULFID DISULFID

BINDING

DOMAIN SIGNAL

HSSb;

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MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 86076906.
REID K.B.M.;
BIOCHEM. J. 231:729-735(1985)
                                                                                                                                                                                                                                                                                                                                                                                      9.9%;
larity 55.6%;
Conservative
                                                                                                                                                                                                                                  EMBL; U04806; G483845; -.
EMBL; U03858; G494979; -.
EMBL; U29874; G1072037; -.
EMBL; U29874; G1072038; -.
                                                                                                                                                                                                                                                                                                                                                      235
72
26416 1
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                                                                                                                                                                                                                                                        EMBL; U29874; G1072038; MIM; 600007; -
CYTOKINE; GLYCOPROTEIN; TSIGNAL 1 26
CHAIN 27 235
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235
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178
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HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                      235 AA;
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 10; Conser
  EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 86076906.
                                                                                                                                       SEQUENCE FROM N.A.
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CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                DOMAIN
TRANSMEM
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Matches
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OF THE COMPLEX. THIS RECEPTOR ALSO BINDS INSULIN GROWTH FACTOR II.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. LYSOSOMAL.
-!- DOMAIN: CONTAINS 1S REPEATING UNITS OF APPROXIMATIVELY 147 AA. THE MOST HIGHLY CONSERVED REGION WITHIN THE REPEAT CONSISTS OF A STRETCH OF 13 AA THAT CONTAINS CYSTEINES AT BOTH ENDS.
PIR; A30788; A30788.
PIRS; PO2784; 1PDC.
PROSITE; PS000023; FIBRONECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                       POTENTIAL.
CATION-INDEPENDENT MANNOSE-6-PHOSPHATE
                                                              ROSITE; PS00023; FIBRONECTIN_2; 1.
RANSMEMBRANE; TRANSPORT; GLYCOPROTEIN; REPEAT; RECEPTOR; LYSOSOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLT3LG.
HOMO SAPIENS (HUMAN).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                           FIBRONECTIN TYPE-II
                                                                                                               LUMENAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                     MW; 1AF70E56 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 94; DB 1; LA
Pred. No. 3.04e-01;
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01-0cT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
SL CYTOKINE PRECURSOR (FLT3 LICAND).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                       RECEPTOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    10.1%;
ilarity 60.0%;
Conservative
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FL3L_HUMAN
P49771;
01-0CT-1996 (
                                                                                                              DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                         DOMAIN
CARBOHYD
CARBOHYD
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CARBOHYD
SEQUENCE
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                                                                                SIGNAL.
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REPEAT
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Matches
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AC P4
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POTENTIAL.
DSSTLPPPWSPRPLEATA -> VETVFHRVSQDGLDLLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ONCOGENE 11:1165-1172(1995).

-1- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING FACTORS AND INTERLEUKINS.

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. A SOLUBLE FORM IS ALSO PRODUCED BY ALTERNATIVE SPLICING.

-1- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE
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                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 94235842.
MEDLINE; 94235842.
MEDLINE; DE VRIES P.,
ESCOBAR S.S., DOWNEY H., SPLETT R.R., BECKMANN M.P., MCKENNA H.J.;
BLOOD 83:2795-2801(1994).
SEQUENCE FROM N.A.
MEDLINE; 94195428.
HANNUM C., CULPEPPER J., CAMPBELL D., MCCLANAHAN T., ZURAWSKI S
HANNUM C., CULPEPPER J., CAMPBELL D., MCCLANAHAN T., LUH .
BAZAN J.F., KASTELEIN R., HUDAK S., WAGNER J., MATTSON J., LUH .
DUDA G., MARTINA N., PETERSON D., MENON S., SHANAFELT A.,
MUDROH M., KELNER G., NAMIKAWA R., RENNICK D., RONCAROLO M.G.,
ZLOTNIK A., ROSNET O., DUBREUIL P., BIRNBAUM D., LEE F.;
NATURE 368:643-648(1994).
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EUTHERIA; PRIMATES.
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LYMAN S.D., STOCKING K., DAVISON B., FLETCHER F., JOHNSON L.,
ESCOBAR S.;
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MISSING (IN ISOFORM).
G -> A (IN REF. 1).
F3F8AB35 CRC32;
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Pred. No. 5.60e-01;
6; Mismatches 2;
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Thu Jul 30 09:02:52 1998; MasPar time 7.57 Seconds 632.140 Million cell updates/sec m ou:

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>US-08-938-548A-2 (1-131) from USO8938548A.pep 931 1 MNLPSTKVSWAAVTLLLLLLL......GRRCSAPAAASVAPGGQSGI 131 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

120441 seqs, 36531193 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d Database:

Mean 39.642; Variance 90.062; scale 0.440 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Pred. No.	1.59e-02	2.13e-02	2.85e-02	2.85e-02	5.09e-02	9.04e-02	1.20e-01	1.20e-01	1.60e-01	1.60e-01	4	2.80e-01	2.80e-01	3.70e-01	3.70e-01	4.88e-01	6.43e-01	6.43e - 01	8.46e-01	1.11e+00	1.11e+00	1.11e+00	. 1.11e+00
Description	prostaglandin G/H syn	prostaglandin-endoper	secretin precursor -	cyclooxygenase 1 - ra	hypothetical protein	tensin - chicken (fra	tensin - chicken	tensin, cardiac muscl	prostaglandin-endoper	prostaglandin-endoper	FLT3/FLK2 ligand (clo	phogrin - human	transmembrane tyrosin	adenylate cyclase (EC	type 5 adenylyl cycla	prostaglandin-endoper	hypothetical protein	hypothetical protein	m	growth-regulated prot	protein-tyrosine phos	protein-tyrosine-phos	mannose 6-phosphate r
£	861698	A36746	SEPG	S39782	A65022	A57075	S27939	A54970	A38146	JH0259	S43293	JC5062	JC5263	A46187	A49201	A35564	S37804	A61183	JC6197	B28414	152599	I38670	A30788
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## ALIGNMENTS

S69198 #type complete prostaglandin G/H synthase 1 - rat prostaglandin G/H synthase 1 - rat #formal_name Rattus norvegicus #common_name Norway rat 24-Avg-1996 #sequence_revision 13-Mar-1997 #text_change 10-Sep-1997 S69198	olecule_type esidues ross-referenc s	ttch 11.7%; Score 109; DB 2; Length 602; cal Similarity 53.6%; Pred. No. 1.59e-02; 15; Conservative 6; Mismatches 5; Indels 2; Gaps 1; LLILLILIPPPPVLITDAGVPSPVNPCC 39           : ::   :   :   LLILLILIPPALLSSGAAAQPLPDCC 40	A36746 #type complete prostaglandin-endoperoxide synthase (EC 1.14.99.1) 1 - human #formal_name Homo sapiens #common_name man 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 29-Aug-1997 A36746 A36746 Xokoyama, C.; Tanabe, T.
REGULT 1 ENTRY TITLE ORGANISM DATE DATE ACCESSIONS REFERENCE #authors #submilssion #accession ##accession ##accession ##accession ##accession	##molecule ##residues ##cross-re #authors #journal #title #accession ##ccession ##residues ##residues ##residues ##residues ##residues ##residues ##residues ##residues	Query Match Best Local S Matches 1 Db 12 LLLL Oy 15 LLLL	RESULT 2 EWTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors

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J. Mol. Biol. (1992) 227:593-595
Occurrence of an actin-inserting domain in tensin.
$28973
                                                                                                                                                                                                                                                                                       Chuang, J.Z.; Lin, D.C.; Lin, S.
J. Cell Biol. (1995) 128:1095-1109
Wolecular cloning, expression, and mapping of the high affinity actin-capping domain of chicken cardiac tensin. A57075
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                                 15 LILILILIDPALLSSGAAAQPLPDCCRQKTCSCRLYELLHGAGNHAAGILILGKRRSGPP 74
                                                                                                                                                         #type fragment
tensin - chicken (fragment)
#formal_name Gallus gallus #common_name chicken
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##residues 862-871,'X',873-875,'A',877-1212 ##label WEI
XY #length 1733 #molecular-weight 186121 #checksum
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submitted to the EWBL Data Library, August 1991
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Pred. No. 1.20e-01;
13; Mismatches 22; Indels
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#authors Diaz, A.; Reginato, A.M.; Jimenez, S.A.
#journal J. Blol. Chem. (1992) 267:10816-10825.
#title Alternative splicing of human prostaglandin G/H synthase mRNA and evidence of differential regulation of the resulting transcripts by transforming growth factor beta 1, interleukin 1 beta, and tumor necrosis factor alpha.
                                                                                                                                            Lo, S.H.; An, Q.; Bao, S.; Wong, W.K.; Liu, Y.; Janmey, P.A.; Hartwig, J.H.; Chen, L.B.
J. Biol. Chem. (1994) 269:22310-22319
Molecular cloning of chick cardiac muscle tensin. Full-length CDNA sequence, expression, and characterization.
A54970
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#formal_name Homo sapiens #common_name man
31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
20-Mar-1998
           tensin, cardiac muscle - chicken
#formal_name Gallus gallus #common_name chicken
11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change
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#length 1744 #molecular-weight 187256 #checksum
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SUMMARY

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Premont, R.T.; Jacobowitz, O.; Iyengar, R.
Endocrinology (1992) 131:2774-2784
Lowered responsiveness of the catalyst of adenylyl cyclase t
stimulation by GS in heterologous desensitization: a role
for adenosine 3',5'-monophosphate-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                              ##status preliminary; not compared with conceptual translation ##molecule_type mRNA #fresidues 1.1165 ##label YOS ##experimental_source NCB-20 cells #experimental_source NCB-20 cells sequence extracted from NCBI backbone (NCBIP:110233) ##note #superfamily guanylate cyclase catalytic domain homology phosphorus-oxygen lyase; transmembrane protein
                                                                        A46187 #type complete adenylate cyclase (EC 4.6.1.1) type V, calcium-inhibitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##experimental_source 849 lymphoma cells
##note
NCBIN:119384,
NCBIP:119386)
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#label GCC\
#domain guanylate cyclase catalytic domain homology
#label GCC2 #domain homology
#label GCC2 #molecular-weight 130318 #checksum 5828
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type 5 adenylyl cyclase - mouse
type 5 adenylyl cyclase - mouse
#formal_name Mus musculus #common_name house mouse
19-bec-1993 #sequence_revision 18-Nov-1994 #text_change
07-Jul-1995
A49201
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#authors Yoshimura, M.; Cooper, D.M.

#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:6716-6720

#title Cloning and expression of a Ca(2+)-inhibitable adenylyl

#cross-references MUID:92357702
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20-Oct-1993 #sequence_revision 18-Nov-1994 a
16-Feb-1997
A46187

    148 SSLTLLMAVLVLLMAVLLTFHAAPAQPQPAYVALLTCASVLFVVL 192

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##molecule_type nucleic acid
##residues 1-1166 ##label PRE
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##cross-references GB:Y08569; NID:g1644377; PID:e273864; PID:g1644378
T This protein has an intracellular protein tyrosine phosphatase like
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#domain transmembrane *status predicted #label TWM\

#domain protein-tyrosine-phosphatase homology #label

PTP2\
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25-Apr-1997 #sequence_revision 09-May-1997 #text_change
24-Oct-1997
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                                            Kawasaki, E.; Hutton, J.C.; Eisenbarth, G.S.
Biochem. Biophys. Res. Commun. (1996) 227:440-447
Molecular cloning and characterization of the human
transmembrane protein tyrosine phosphatase homologue,
phogrin, an autoantigen of type 1 diabetes.
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ICAAR, a novel member of a new family of transmembrane,
tyrosine phosphatase-like proteins.
JC5263
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    #binding_site substrate phosphate (Arg) #status
    predicted
#length 1015  #molecular-weight 111280 #checksum 4788
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predicted\
#binding_site substrate phosphate (Arg) #status
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##cross-references GB:U66702; NID:g1620663; PID:g1620664
FICATION #superfamily protein-tyrosine-phosphatase homology
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>US-08-938-548A-2 (1-131) from USO8938548A.pep 931 1 MNLPSTKVSWAAVTLLLLLL......GRRCSAPAAASVAPGGQSGI 131 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

63816 seqs, 5850866 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5\_COMB 2:PCT9\_COMB 3:backfiles

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 27.627; Variance 133.583; scale 0.207

Statistics:

#### SUMMARIES

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Patent No. 5212074.  Patent No. 5258287.  Sequence 14, Applicatio Sequence 10, Applicatio Sequence 13, Applicatio Sequence 2, Applicatio Sequence 3, Applicatio Sequence 3, Applicatio Sequence 5, Applicatio		1337 AA.		d stman, Arne inced Protein Tyrosine Gerstein, Murray & ,, Suite 6300	, Version #1.25 512 31954 CN;
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GENERAL INFORMATION:
APPLICANT: CHAMBON, PIERRE
APPLICANT: BASSET, PAUL
APPLICANT: BASSET, PAUL
APPLICANT: BASSET, PAUL
APPLICANT: BELLOCQ, JEAN-PIERRE
TITLE OF INVENTION: CANCER
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Ave. NW Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
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CLASSIFICATION NUMBER: 05/07/794,393
FILING DATE: 1991121
APPLICATION NUMBER: 08 9025326.1
APPLICATION NUMBER: 08 9025326.1
APPLICATION NUMBER: 29,021
REGISTRATION NUMBER: 29,021
RECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
JENCE 492 AA; 55340 MW; 1261070 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application PC/TUS9405365
                                                                                                                                                                                                    Sequence 4, Application US/07794393
Patent No. 5236844
                                                                                                                                                                      Sequence 4, Application US/07794393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 LLLLLLLPSPLMARARPPES 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 LILLILLIPPALLSSGAAAQP 35
 15 LLLLLLLPPALLSSGAAAQP 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 20036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US94-05365-2
                                                 LT 5
US-07-794-393-4
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                                                 RESULT
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08001711
Patent No. 5484726
GENERAL INFORMATION:
APPLICANT: BASSET, PAUL
APPLICANT: BLICOCO, JEAN-PIERRE
APPLICANT: CHAMBON, PIERRE
TITLE OF INVENTION: ANALYTICAL MARKERS FOR MALIGNANT BREAST
TITLE OF INVENTION: CANCER
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                Score 92; DB 2; Length 235;
Pred. No. 6.53e+00;
6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
9.8%; Score 91; DB 1; Length 492;
Best Local Similarity 47.6%; Pred. No. 7.65e+00;
Matches 10; Conservative 9; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1225 Connecticut Suite 300
CITY: Washington
STATE: D.C.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: BAPC Compatible
COMPOTER: BAPC COMPATIBLE
SOFTWARE: PSPELICATION ANGER: US/08/001,711
FILING DATE: 19930107
FILING DATE: 19930107
                                                                                                                                                                                                                                        492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MILLMAN, ROBERT A
REGISTRATION UNDBER: 36,217
REFERENCE,/DOCKET UNDBER: 1383.0040001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/794,393
FILING DATE: 11-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9025626.1
FILING DATE: 21-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
JENCE 492 AA; 55340 MW; 1261070 CN;
               MOLECULE TYPE: protein
JENCE 235 AA; 26415 MW; 293990 CN;
                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08001711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202)833-8716
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 492 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 LLLLLLLPSPLMARARPPES 42
                                                                                                                                                                                                                                        STANDARD;
                                                               Query Match 9.9%;
Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                                      9 SWAAVTLILLLIPPAL 26
                                                                                                                                   7 AWSPITYLLLLLLSSGL 24
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                          T 4
US-08-001-711-4
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                               SEQUENCE
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Gaps

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APPLICANT: BECKMANN, M. P.
APPLICANT: BECKMANN, M. P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
                                APPLICANT: Nocka, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
TITLE OF INVENTION: FLI-3/FLK-2 LIGAND
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03866
Inc. (all states except US)
if (US only)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: US 08/220,379
FILING DATE: 28-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/POCKET WUMBER: Cytomed/2
                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
COUNTRY: New York
COUNTRY: United States of America
ZIP: 10020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein
LOCATION: 1..205
ICE 231 AA; 25999 MW; 274601 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.6%; Score 89; Best Local Similarity 57.9%; Pred. No. Matches 11; Conservative 5; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMUNEX CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08240124
Patent No. 5516658
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08240124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELERA: 212-200. INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 AWSPNSSLLLLLLLLSPCL 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-240-124-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XXXXX
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                                                                                 APPLICANT: Lyman, Stewart D.
APPLICANT: Lyman, M. Patricia
TILLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 231;
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,545
FILING DATE: 11.MAX-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: MAY 24, 1993
CLASSIFICATION: A35
ATORNEY/AGENT INFORMATION:
NAME: MAIBARA, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
SEQUENCE 231 AA; 26027 MW; 272421 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application PC/TUS9503866 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application PC/TUS9503866
     Sequence 2, Application US/08243545
Patent No. 5554512
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (206) 587-0430
(206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 231 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.6%;
ilarity 57.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 SWAA-VILLLILLIPPAL 26
                                                                                                                                                                                                                                                                                                                        Washington : US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US95-03866-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                        STATE: Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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Query Match

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APPLICANT: Goodearl, Andrew; Stroobant, Paul;
APPLICANT: Goodearl, Andrew; Stroobant, Paul;
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
APPLICANT: Chen, Maio Su; Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their
TITLE OF INVENTION: Preparation and Use
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREE: 805 Third Avenue
CITY: New York City
STRIE: New York City
STRIE: New York City
COUNTY: USA
LIP: 100.2
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                  Score 86; DB 1; Length 202, Pred. No. 1.68e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                      422 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCHWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,569
ELING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: US/08/69,569
PRIOR APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 330-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY DATE: 10-APRIL-1991
ATTORNEY/AGENT INFORMATION:
RAME: Tsai, Christine H.
REGISTRATION NUMBER: 34,266
REPERENEL/COCKET NUMBER: LUD 5250.4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
LENGTH: 254 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 254 AA; 26624 MW; 316872 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 170, Application US/08469569
Patent No. 5606032
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 170, Application US/08469569
                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 03-APRIL
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                       Query Match 9.2%;
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                         S VSWAAVTLLLLLLPPA 25
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DE Sequence 170, Applic XX

CONTROLLICANT: Goods CONTROLLICAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 51 University Street
CITY: Seattle
STATE: Washington
TIP: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 88; DB 1; Length 1165
Pred. No. 1.23e+01;
14; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 SSLTLLMAVLVLLTAVLLAFHAAPARPQPAYVALLACAATLFVAL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 AAVILLI-LILILIPPALLS-SGAAAQPLPDCCRQKICSCRLYELL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 7.5.3
SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
ETLING DATE: 06 May-1994
                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
FENCE 1165 AA; 130394 MW; 6766222 CN;
APPLICATION NUMBER: US/08/240,357
FILING DATE: 10-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08236918A
Patent No. 5674704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08236918A
                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30,637
REFRENCE/DOCKET NUMBER: 31,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3244
                                                                                                                                  30,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION
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REGISTRATION NUMBER: 32,17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (206) 587-0430
                                                                                                                                                                                                                                    TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                               201-831-330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 9.5%;
Local Similarity 33.3%;
les 15; Conservative
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                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 07 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-236-918A-4
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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(MI)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:02:10 1998; MasPar time 5.32 Seconds 377.841 Million cell updates/sec on:

(1-131) from US08938548A.pep 931 1 MNLPSTKVSWAAVTLLLLLL......GRRCSAPAAASVAPGGQSGI 131 >US-08-938-548A-2 rabular output not generated. Description: Perfect Score: Sequence: Title:

Scoring table:

PAM 150 Gap 11

Searched:

124785 segs, 15338987 residues

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq31-2 Database:

iparti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part27

Mean 29.691; Variance 135.127; scale 0.220 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

No.	Score	Query	Query Match Length DB	DB	e e	Description	Pred. No
П	108	11.6	599	4	R21690	Prostaglandin endoper	1.04e+00
7	66	10.6	696	24	W25170	Human insulinoma-asso	4.77e+00
m	66	10.6	986	74	W25171.	Human insulinoma-asso	4.77e+00
4	66	10.6	1012	56	W35296	Macaque islet cell an	4.77e+00
Ŋ	66	10.6	1015	27	W35345	Human protein tyrosin	4.77e+00
9	66	10.6	1015	23	W18092	Type I diabetes assoc	4.77e+00
7	94	10.1	1337	14	R85203	huder-1.	1.09e+01
æ	92	9.9	235	12	R67541	Human flt-3 ligand.	1.52e+01
6	92	6.6	235	13	R66175	Human S86/S109 F1t3 1	1.52e+01
10	91	9.6	492	'n	R24863	Sequence of pre-pro s	1.78e+01
11	88	9.6	35	-	P94256	Truncated E protein f	2.47e+01
12	89	9.6	231	12	R67540	Mouse flt-3 ligand.	2.47e+01
13	89	9.6	232	13	R66177	Mouse MoT110/T118 Flt	2.47e+01
14	88	9.5	234	91	R82605	Eph transmembrane tyr	2.90e+01
15	88	9.5	238	13	R71481	Human hek-L protein.	2.90e+01
16	88	9.5	480	53	W22849	Osteoblast like cell	2.90e+01
17	88	9.5	1165	7	R37309	Cardiac adenylyl cycl	2.90e+01
18	87	9.3	186	9	R32428	Wheat germ agglutinin	3.40e+01
19	87	6	551	13	R77858	S. clayuliderus ORF1	3 400+01

3.99e+01 3.99e+01 3.99e+01 3.99e+01 4.68e+01 4.68e+01		4	4.68e+01 4.68e+01 5.49e+01 5.49e+01 5.49e+01
agland.5 frag. 4-1BB 4-1BB 28 gen. n glial	gilal growth gment E. gment E. gment E. e complement eligilal cell gro	neuregulin encoded by growth fact hGGF2. GGF2. growth fact growth fact	GGF-II encoded by clo C. acidovorans stereo Murine interleukin-15 Insulin-like growth f Wzy (Rfc) protein inv Human DOCK180 protein
P91008 R50054 W26657 R64190 W03740 W09358	K6/445 R55653 R96074 R46912 W12414 R67258	M09371 R46923 R87467 W09372 R87466	R55654 R31036 R90840 R89952 W37355
78777887	123 17 62	10 11 11 11 11 11 11 11 11 11 11 11 11 1	9 119 132 130
126 126 254 254 1481 248 248	2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	422 426 263 291 438 1865
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#### ALIGNMENTS

The protein sequence of hPES was deduced from the cDNA sequence obtd. by screening a human genomic library in EMBL3. hPES can be used to screen anti-inflammatory agents. An anti-body against a peptide specific to hPES can be made, and used for the determination of the protein.

Sequence 599 AA; Human prostaglandin endo-peroxide synthase – for screening antiinflammatory agents Claim 1; Page 1; 10pp; Japanese. Length 599; R21690; 23-JUL-1992 (first entry) Prostaglandin endoperoxide synthase. Human; hPES; screening; anti-inflammatory; antibody. JO4045786-A. T 1 R21690 standard; Protein; 599 AA. 14-FEB-1992. 13-JUN-1990; 152784. 13-JUN-1990; JP-152784. (MEIP.) MELGI MILK PRODS KK. WPI; 92-101937/13. N-PSDB; Q23001 RESULT 

Gaps ij 7; Indels Score 108; DB 4; 1 Pred. No. 1.04e+00; 4; Mismatches Query Match 11.6%; Best Local Similarity 55.6%; Matches 15; Conservative

ä

15 LLLLLLLP-PALLSSGAAAQPLPDCC 40 JT 2 W25170 standard; Protein; 969 AA. οχ

10 lllllllpplpvlladpgaptpvnpcc 36

g

W25170; 15-DEC-1997 (first entry) Human insulinoma-associated antigen 2-beta (short version). Insulinoma-associated antigen 2 beta; IA-2 beta; autoantigen; insulin dependent diabetes; IDD; antibody; diagnosis; susceptibility; 

type 1; type 2. Homo sapiens. WO9707211-A1.

Domain Domain Domain

Region

```
Novel islet cell antigen-related protein tyrosine phosphatase resequising auto-antibodies associated with insulin useful for recognising auto-antibodies associated with insulin dependent diabetes mellitus

Claim 4: Page 57-63; 67pp; English.

Human islet cell antigen-related protein tyrosine phosphatase

CI (RR-PPP) (WI8092) has the properties of an insulin-dependent

Ci (RR-PPP) (WI8092) has the properties of an insulin-dependent

Ci (alabetes mellitus (IDDM)-associated autoantigen. Its amino acid

sequence was deduced from CDNA clones (T67296) obtd. from human

compared and brain cDNA libraries. Complete, partial (see also

WI8091) and cytoplasmic region (see also w18093) IRR-PTP

CO propeptides can be produced using host-vector systems and used,

CO either as an alternative to autoantigen IA-2 or in combination with

IR-2, for the diagnosis of IDDM, e.g. to screen for or predict the

CO conset, presence or development of IDDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 34-38; Sipp; English.
A cDNA clone was obtd. (see T06027) from a HeLa cell cDNA library that encoded a novel density-enhanced Type III receptor-like PTP, designated hubEp-1 (R85203). hubEp-1 is useful for the study of PTPs and for the development of therapeutic or prophylactic cpds. e.g. for prevention of abnormal or malignant cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-FBB-1996 (first entry)
hubEP-1.
Density enhanced Type III receptor-like protein tyrosine phosphatase;
hubEP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New density enhanced protein tyrosine phosphatase - used to develop prods. to modify transcription, translation and/or activity of tyrosine phosphatase(s).
                                                                                                                                                                                                                                                                                                                                              /label- Glycosylation
/note- "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.6%; Score 99; DB 23; Length 1015;
larity 57.1%; Pred. No. 4.77e+00;
Conservative 7; Mismatches 2; Indels (
                                                                                       22..614
/label= Extracellular_domain
                                                                                                                                                     615..639
/label- Transmembrane_domain
                                                                                                                                                                                                                   640..1015
/label= Intracellular_domain
label Sig_peptide
                                                          /label- Mat_protein
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03-MAY-1995.
03-MAY-1994; US-237940.
(COLD-) COLD SPRING HARBOR LAB.
OSSTHAM A, TONKS NK;
WPI: 95-393079/50.
N-PSDB: T066027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-1995; GB-026036.
19-MAR-1996; GB-005710.
27-SEP-1996; GB-020265.
(UXSI-) UNIV SINGAPORE NAT.
                          ..1015
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ses 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUN-1997.
20-DEC-1996; CA0867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 97-341685/31.
N-PSDB; T67296.
                                                                                                                                                                                                                                                                                    active_site
modified_site
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WO9530008-A1.
                                                                                                                                                                                                                                                                                                                                                                                                               WO9722694-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pallen CJ;
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                                protein
                                                                                              domain
                                                                                                                                                                                                                         domain
                                                                                                                                                            domain
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 97-503042/46.

R WPI; 97-503042/46.

R Protein tyrosine phosphatase MOT12 - used to develop products for the diagnosis and treatment of, e.g. cell proliferative disorders.

T diabetes and immune disorders

Claim 9: Fig 1: 64pp; English.

This protein sequence comprises a novel human receptor-type protein tyrosine phosphatase, designated MOT12, suggested to play a role in the growth, differentiation and survival of neurons in the adult. The amino acid sequence was deduced from a coding sequence (see 195368) of overlapping cDNA clones isolated from the adult. The amino acid sequence was deduced from a coding sequence (see 195368) of overlapping cDNA clones isolated from candate nucleus and pancreas cDNA libraries. MOT12 expression is highly restricted, being found only in adult brain and pancreas in neurosecretory cell types. Polypeptides, including those that comprise residues 1-614, 615-706 or 707-1082 of MOT12 or comprise MOT12 lacking one or more of the extracellular, transmembrane or intracellular domains, can be expressed in methods transgenic animals and antibodies can be used in methods transgenic animals and antibodies can be used in methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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14-SEP-1997 (first entry)
Type I diabetes-associated autoantigen IAR-PTP.
Insulin dependent diabetes mellitus-associated autoantigen; IDDM;
islet cell antigen-related protein tyrosine phosphatase; IAR-PTP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for the treatment, diagnosis and screening of MOT12-related diseases or conditions characterised by an abnormal interaction between MOT12 and a natural binding partner, especially diabetes an immune disorder or cancer (claimed).
                                                                                                                                                                                                                                                                             /note- "residue 294 is Glu in protein encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "predicted phosphotyrosine contact site" 776..779 /note= "predicted rim of binding pocket"
                                                                                                                                                                                                                                                                                                                                                                               note- "predicted phosphotyrosine contact site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note- "predicted base of binding pocket"
911..919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "predicted surface loop"
                                                                                                                                                                                                                                                                                                              a pancreas cDNA clone"
                                                                                                              615..706
/note= "transmembrane domain"
                                                                                                                                                                               707..1082
/note= "intracellular domain"
                                                                                    "extracellular domain"
                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W18092 standard; Protein; 1015 AA.
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/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-1997; U05284.
25-MAR-1997; US-816962.
29-MAR-1996; US-014267.
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Matches 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                   Misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                               Misc_difference
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   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Binding_site
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Location/Qualifiers 1..21

peptide

Key

RESULT ID WI AC WI DOT 14 DE TY KW IS KW DS CON HELD CON

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Gaps

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RESULT
ID P9
AC P9
DT 10
DT 13
DE Tr
KW E
PN WO

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Navigand for the Flt3 tyrosine kinase receptor - and related nucleic acid, vectors, host cells and antibodies, useful for treating abnormal cell physiology and proliferation, e.g. cancer, also for diagnosis and drug screening.

Tolaim 11: page 79-80; 90pp; English.

A cDNA library from the human stromal cell line 29SV48, in pwEl8S, was screened with an 800 bp fragment derived from mouse clone T118. This fragment encompasses the coding region conserved between two mouse clones, T118 and T110. Approx. 20 positive clones were selected and partially sequenced. Two clones, S86 and S109, were found to be approx. 75% homologous to the mouse clones over the first 163 AAs. Clone S86 continued clones, S86 and S109, were found to be approx. 75% homologous clones, s86 and s109, were found to be approx. 75% homologous clones solver the first 163 AAs. Clone S86 continued clones were degree, for an overall homology of 66%. Clones T118 and selected mouse residue 163 (human residue 160). An additiona mouse the common and divergent portions of the mouse ligand. Sequence 232 AA;
                                                                                       Insolated ligands for flt 3 receptors - useful for treating anaemia, AIDS and various cancers Disclosure; page 25-7; 33pp; English.

CDNA encoding mouse flt3-ligand (flt3-L) was isolated from a CDNA library of T-cell line P7B-0.3A4 in CV-1/EBNA-1 cells using a slide autoradiography method. Flt3-L stimulates production of progenitor and stem cells, and can be used e.g. Sequence 231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 89; DB 13; Length 232;
Pred. No. 2.47e+01;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                       Length 231;
                                                                                                                                                                                                                                                                                       Score 89; DB 12; Length 231 Pred. No. 2.47e+01; 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-AUG-1995 (first entry)
Mouse MoT110/T118 Flt3 ligand peptide fragment.
Flt3 ligand; tyrosine kinase receptor ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee FD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-NOV-1994.

18-NAY-1994.

19-NAY-1993. US-065231.

07-UL-1993. US-089263.

16-JUL-1993. US-082549.

16-JUL-1993. US-106340.

24-NG-1993. US-112391.

19-NOV-1993. US-112391.

(INRM) INST NAT SAWTE & RECH MEDICALE.

(SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birnbaum D, Culpepper JA, Hannum CH, WPI; 95-006787/01.
N-PSDB; Q79464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R66177 standard; Peptide; 232 AA.
                                                                                                                                                                                                                                                                                       Query Match 9.6%;
Best Local Similarity 57.9%;
Matches 11; Conservative
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Best Local Similarity 57.9%;
Matches 11; Conservative
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                                 Beckmann MP, Lyman SD;
WPI; 95-008071/02.
N-PSDB; Q79076.
               (IMMV) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
11-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R66177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating or preventing microbial infections - using cecropin(s), attacin(s), lysozyme(s), S protein from lambda phage, E protein from pHI x174 or protein from phage 22.

Claim 108; page 58; 64pp; English.

The truncated E protein is an antimicrobial polypeptide. DNA encoding the protein is used to transform animal cells to express the protein, proteins may also be admin. to humans and animals for preventing or transforms, eg brucellosis, malarial infection. The proteins may also be admin. to humans and animals for preventing or transforms, eg brucellosis, malarial infection, see also P94254-P94258.
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06-JUL-1987; US-069653.
(LOUT) Louisiana State University Agricultural and Mechanical College.
Jaynes JM, Enright FM, White KL;
WPI; 89-039653/05.
                                                         Gaps
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R67540 standard; Protein; 231 AA.
R67540;
05-MG-1995 (first entry)
Mouse fit-3 ligand.
Fit-3 ligand; fit3-L; anemia; cancer; AIDS; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 492;
                                                     2; Indels
             re 91; DB 5; Le
d. No. 1.78e+01;
Mismatches 2;
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/label= Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189..211
/label- Transmembrane_domain
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/label- Cytoplasmic_domain
                                                                                                                                                                                                                                               10-JUN-1997 (revised)
13-JUN-1990 (first entry)
Truncated E protein from Phix174.
E protein; antimicrobial agent; Phix174.
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                   Score
                                   Pred.
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P94256 standard; protein; 35 AA
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                                                                                                               15 LILLILLEPPALLSSGAAAOP 35
             Query Match
Best Local Similarity 47.6%;
Matches 10; Conservative
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Best Local Similarity 55.6%;
Matches 10; Conservative
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10 WAAVTLLLLLLLPPALL 27
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US-106463.
US-111758.
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US-209502.
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                                                                                                                                                                                                                              P94256;
10-JUN-1997
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07-MAR-1994;
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:33:36 1998; MasPar time 3.35 Seconds 128.334 Million cell updates/sec bular output not generated. no un

>US-08-938-548A-12 (1-28) from US08938548A.pep 201 1 RPGPPGLQGRLQANGNHAAGILIM 28

Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

124785 seqs, 15338987 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

1.part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 20:part20 21:part21 22:part22 23:part22 23:part25 26:part26 27:part27 a-geneseq31-2

Mean 22.110; Variance 87.356; scale 0.253 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

)		dР				٠	
Result No.	Score	Query	Query Match Length DB	DB	ΙD	Description	Pred. No.
н	89	33.8	2192	23	W21732	LexA/NuMA fusion prot	4.36e+01
7	68	33.8	2272	23	W21731	GAL4/HA/NuMA fusion p	4.36e+01
m	99	32.8	10	4	R20235	"p33" N-terminal (2).	6.36e+01
4	9	32.3	716	18	R99737	Retinoid X receptor i	7.68e+01
S	65	32.3	2509	24	W32881	Protein (OA-519) cros	7.68e+01
9	64	31.8	256	σ	R45403	Deduced sequence of h	9.25e+01
7	64	31.8	256	12	R85639	MY17 preproPR-3.	9.25e+01
80	64	31.8	549	16	R92050	KM31-7 precursor.	9.25e+01
σ	64	31.8	1477	13	R67691	S. cerevisiae scaur2R	9.25e+01
10	64	31.8	1477	55	W10424	Saccharomyces cerevis	9.25e+01
11	63	31.3	878	ø	R32889	DHR23alpha protein.	1.11e+02
12	63	31.3	878	ო	R13793	Ecdysone receptor.	1.11e+02
13	63	31.3	1841	52	W22605	Tylactone synthase OR	1.11e+02
14	63	31.3	4630	22	W19629	Streptomyces venezuel	1.11e+02
15	62	30.8	684	24	W26327	Human alpha-1 collage	1.34e+02
. 16	61	30.3	32	7	R00579	New polypeptide based	1.61e+02
17	61	30.3	248	П	R04216	Human 32K ASP encoded	1.61e+02
18	61	30.3	248	Н	P82980	Sequence deduced from	1.61e+02
19	19	30.3	248	m	P60666	Genomic sequence of h	1.61e+02

2192 AA;

Sequence

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1. 61e+02 1. 61e+02
Plasmid pASPC-SV(10) Human alveolar surfac Human 32K ASP encoded Sequence deduced from 35kd pulmonary surfac 35kd pulmonary surfac Sequence of human alv Plasmid pASPCq-SV(10) Vector PSP 35K-1A-10 Human 32K alveolar su Genomic Sequence of h Human 32K ASP encoded Human adipogenesis in Human adipogenesis in Human interleukin-11 Human interleukin-11 Human interleukin-11 Human interleukin-11 Human interleukin-11 Human interleukin-11 Human madipogenesis in Human salpogenesis in Human interleukin-11 Human interleukin-11 Human macipogenesis in Human pacipogenesis in Human macipogenesis in Human Ras-related pro Thermus aquaticus hea Virulence-associated Human focal adhesion
P60441 R06331 R06531 P804215 P70663 P70663 P70663 P70663 R04212 R04212 R04212 R04212 R04212 R04212 R04212 R04212 R04212 R04212 R04212 R04212 R04213 R1533 R1533 R1533 R1543 R16812 R16812 R16812 R16813 R1681
11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
248 2488 24488 24488 24488 24488 2488 2
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## ALIGNMENTS

	U-OCT-1997 (litrst entry)  LexA/NUMA fusion protein.  NIP-1; NIP-2; NUMA; nuclear mitotic apparatus; NUMA interacting protein;  LexA/NUMA fusion protein.  NIP-1; NIP-2; NUMA; nuclear mitotic apparatus; NUMA interacting protein;  malignant cell growth.  Homo saplens.  Location/Qualifiers  Gomain  Alabel = LexA_DNA_binding_domain  Rey  Los   1.87
ខ្លួ	which may be markers for aberrant (including malignant) cell growth
36	(Which can also be detected by notities sequencing). Also where maniforms is white the defeated by notities and the treated by
ပ္ပ	malignancy is related to defects in NuMA or NIP, it can be treated by
ָ נ	administration of the appropriate functions are
ر د	administration of the appropriate innectional protein.

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rppspalasvllalllsgaaraaeiv 29
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Best Local Similarity 38.5%;
Matches 10; Conservative
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02-MAR-1995; U02513
processing.
Sequence 256 AA;
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MY17 preproPR-3
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ID R9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding protein cross-reactive with hpr gene product - useful to raise antibodies reactive with epitope(s) found on hpr gene product, useful in cancer, especially breast cancer, prognosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cpds. which inhibit formation of mature tumour necrosis factor from its precursor - identified using TNF convertase, e.g. mutain(s), antibodies or peptide phosphonate(s), for preventing and treating sepsis, AIDS, auto-immune disease etc. Disclosure; Fig 2; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Columns 43-60; 68pp; English.#
The present sequence is a protein (OA-519) cross-reactive with the haptoglobin related (hpr) gene product. OA-519 can be used raise antibodies reactive with epitopes found on the hpr gene product, but not on haptoglobin 1 or 2, useful in cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                 Protein (OA-519) cross-reactive with hpr gene product.
OA-519; cross-reaction; haptoglobin related; hpr; antibody;
epitope; haptoglobin 1; haptoglobin 2; cancer; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUL-1994 (first entry)
Deduced sequence of human proteinase-3 (PR-3)
TNF convertase; proteinase-3; PR-3; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JAN-1994.
25-JUN-1993; U06120.
25-JUN-1992; US-905546.
(CETU ) CETUS ONCOLLOGY CORP.
Halenbeck RF, Jewell DA, Koths KE, Kriegler M, Perez C;
WPI; 94-026195/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 32.3%; Score 65; DB 24; Length 250
Best Local Similarity 29.6%; Pred. No. 7.68e+01;
Matches 8; Conservative 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       especially breast cancer, prognosis assays. Sequence 2509 AA;
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                                                                                                                                                                                                                                                                                                              24-JUL-1992; US-917716.
26-JUL-1993; US-916908.
05-JUN-1995; US-469008.
(UVJO ) UNIV JOHNS HOPKINS.
KUMPIGA FP. PASTERNACK GR;
WPI: 97-469516/43.
N-PSDB; T88206.
                                                                                                 proquosis assay
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WO9400555-A.
                                                                                                                          Homo sapiens.
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26-JUL-1991;
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treatment of septic shock, Theumatoid arthritis, From.

Example 2; Page 82; 96pp; English.

Contract sequence represents the preproper 3. PR-3 is a active recombinant human neutrophil protease-3. PR-3 is a serine protease, and is a tumour neutrophil protease-3. PR-3 is a serine protease, and is a tumour neutrophil protease-3. PR-3 is a serine protease, and is a tumour necrosis factor alpha (TNFalpha) convertase. The cDNA encoding this conscribed from the HL60 cell clone MX17. The mature PR-3 can be used in the method of the invention for identifying agents that the invention for identifying agents that the protopha to mature TNFalpha. In the method, the cleavage of proTNFalpha is measured by a colourimetric assay.

Che cleavage of the proTNFalpha is measured by a colourimetric assay.

Chis is then repeated in the presence of a test compound that is thought to inhibit this process. The results of the two reactions are then compared to determine whether the test compound is an inhibitor. The cleavage inhibitors can be used in the treatment of septic shock, rheumatoid arthritis, cachexia, cerebral malaria, ischaemia/reperfusion injury, graff-host disease, autoimmune diseases, and AIDS. PR-3 can be used to treat unwanted B cell/T cell interaction by contacting it with Sequence 256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PR-3; preprofices; MY17; human neutrophil protease-3; serine protease; tumour necrosis factor alpha; TRValpha; HL60; MY17; B cell; T cell; tumour necrosis factor alpha convertaes; cytokine; septic shock; rheumatoid arthritis; cachexia; cerebral malaria; graft-host disease; ischaemia/reperfusion injury; autoimmune disease; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - useful for
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                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-1994; US-208574.

19-ARR-1994; US-230428.

27-FBE1995; US-395456.

(CETU ) CETUS ONCOLOGY CORP.

Halenback RF, Jewell DA, Koths KE, Kriegler M, Perez C;

WPP: 95-328287/42.

N-PSDB; T02565.
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   Length 256;
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                                                                      9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identification of inhibitors of mature INFalpha prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "dipeptide present in proPR-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 64; DB 15; I Pred. No. 9.25e+01;
Score 64; DB 9; L
Pred. No. 9.25e+01;
7; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "mature PR-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                  1 RPGPPGLOGRLORLLOANGNHAAGIL 26
                                                                                                                                          4 rppspalasvilalilsgaaraaeiv 29
                                                                                                                                                                                                                                                                                                            n 7
R85639 standard; Protein; 256 AA.
Query Match 31.8%;
Best Local Similarity 38.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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/note= "c
28..256
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production of tylosin-related polyketide compounds claim 9; Pages 103-109; 220pp; English.

Claim 9; Pages 103-109; 220pp; English.

Wa2601-Wa22605 represent proteins encoded by the tylactone synthase gene cluster of the invention. The gene cluster is also referred to as the tyla gene, and was isolated from Streptomyces fradiae. These sequences are multifunctional proteins which direct the synthesis of the polyketide tylactone, isolated from Streptomyces fradiae. Tylactone is the basic building block of the antibiotic tylosin. The DNA sequence can be modified so as to alter the type of carboxylic acids incorporated, the number of carboxylic acids incorporated and/or the post-condensation reactions performed, thereby resulting in novel tylosin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 55; Fig 23; 91pp; English.

3 Polypeptide sequences (W19629-30 and W00918) can be deduced from the vep ORT1 polyfectide synthase (PKS) gene cluster (T68715) of Streptomyces venezuelae. The sequence data indicate that the PKS gene cluster encodes a polyene of 12 carbons. The vep gene cluster contains 5 PKS modules, plus a 5' loading module and a 3' end domain. Each of the sequenced modules includes a keto-ACP, an acyltransferase, a dehydratase, a keto-reductase and an acyl carrier protein domain. A novel expression cassette encoding the first module from the vep gene cluster and module 7 from the Streptomyces trylp gene cluster has polyhydroxyalkanoate (PHA) monomer synthase activity and can be used for PHA prodn. In host (esp. insect) cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expression cassettes for production of polyhydroxyalkanoate(s) provide wide range of biodegradable polymers for medical or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 63; DB 25; Length 1841;
Pred. No. 1.11e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces venezuelae polyketide synthase.
Polyketide synthase; polyhydroxyalkanoate monomer synthase;
polyhydroxybutyrate; biodegradable polymer; vep gene;
metabolic engineering.
                                                                                                      'note= "acyl carrier protein domain, ACP7"
  /note= "acyltransferase domain, AT7"
1171..1355
                                                            /note= "ketoreductase domain, KR7"
1443..1526
                                                                                                                        1663..1695
/note= "thioesterase domain, TE7"
                                                                                                                                                                                                                                                                                  Sutton KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Mismatches
                                                                                                                                                                                                                                                                                  Rosteck PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1513 rdtpaalaahlaellatardhgpg 1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for use as a biodegradable polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J 14
W19629 standard; Protein; 4630 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Williams MD, Xue Y;
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Local Similarity 33.3%;
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01-SEP-1997 (first entry)
                                                                                                                                                                                                                                                          (ELIL ) LILLY & CO ELI.
Dehoff BS, Kuhstoss SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
581..913
                                                                                                                                                                                                           19-FEB-1997; 301056.
22-FEB-1996; US-012078.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-1997.
18-DEC-1996; U20119.
19-DEC-1995; US-008847.
(MINU ) UNIV MINNESOTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1841 AA;
                                                                                                                                                                                                                                                                                                  WPI; 97-418046/39.
N-PSDB; T80413.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; T68715
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                                                                                                                                                                     EP-791655-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sherman DH,
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                                                                                                                                                                                                27-AUG-1997
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                                          Domain
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  Domain
                                                                                    Domain
                                                                                                                               Domain
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             Ecdysteroid dependent regulation of genes in mammalian cells - for induced expression of heterologous genes
Disclosure; Fig 1; 45pp; English.
This sequence represents an ecdysteroid receptor DRR23alpha. DHR23-
alpha is a Drosophila steroid receptor homologue which can function as
a ligand-dependant transcription factor in mammalian cells when induced
by specific ecdysteroids such as DHR23alpha. The activity of DHR33-
alpha is induced upon administration of certain ecdysteroids but not
any of the mammalian hormones tested. DHR23alpha has been reported to
                                                                                                                                                                                                             regulate transcription of genes containing ecdysone response elements
in Drosophila tissue culture cells treated with 20-0H ecdysone.
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tylactone synthase ORF5 protein.
Tylactone synthase gene cluster; tylG gene; multifunctional protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding insect steroid receptors - and ligands, for use as benign inducing factors
claim 24; Page 103; 126pp; English.

The amino acid sequence codes for the (20-0H) ecdysone receptor protein which is part of the insect steroid receptor superfamily. It can be used to screen for ligands specific for the insect steroid receptors which can be used as highly specific and highly active pesticides which are biodegradable. See also R13791-R13794.
                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 878;
                                                                                                                                                                                                                                                                                                    Length 878;
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Pred. No. 1.11e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polyketide; tylactone synthesis; antibiotic; tylosin
Streptomyces fradiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431..651 /note= "hormone-binding domain E"
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                                                                                                                                                                                                                                                                                                    Score 63; DB 6; I
Pred. No. 1.11e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ecdysone receptor.
Insect steroid receptor; EcR; hormone; DHR23.
                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-1990; US-485749.
(STRD ) LELAND STANFORD JR UNIV.
Hogness DS, Koelle MR, Segraves WA;
WPI; 91-281480/38.
N-PSDB; Q13574.
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264..329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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W22605 standard; Protein; 1841 AA.
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R13793 standard; Protein; 878 AA.
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larity 64.3%;
Conservative
                                                                                                                                                                                                                                                                                                    Query Match 31.3%;
Best Local Similarity 64.3%;
Matches 9; Conservative
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15-FEB-1991; U01189
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                                                                                                                                                                                                                                                            Sequence
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W22605;

RESULT

Matches

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R13793;

RESULT

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domain domain

CCCSTTRAN

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Gaps

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8; Indels

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Novel human type alpha-1 (XVIII) collagen is characterised by triple helical domains containing the GXVGX'Y' motif (where X, Y, X' and Y' represent any amino acid), the helical domains being separated and flanked by non-triple helical regions which may provide flexibility. Alpha-1 collagen is expressed in multiple tissues. especially liver, lung and kidney. A claimed plasmid comprising alpha-1 collagen nucleic acid (see T84484) and an expression control sequence can be used to express recombinant collagen in prokaryotic or eukaryotic (especially mammalian) host cells. The alpha-1 collagen may be used to treat a patient suffering from a disease associated with cartilage degradation, and for supplementing collagen. It can also be used as a connective tissue filler (e.g. for plastic surgery), can be interposed between a dermal equivalent and skin to improve adhesion, and as a substrate on which to grow epithelium. The addition of glycosans makes alpha-1 collagen a better carrier for fibroblast growth factor, and imparts greater tensile strength.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding human alpha-1 collagen - for production of recombinant alpha-1 collagen, for use in the treatment of cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    r,_motif
                                        329..334
/label= GXYGX'Y'_motif
/note= "Claim 1"
                                                                                                                 335..340
/label= GXYGX'Y'_motif
/note= "Claim 1"
                                                                                                                                                                                                                                                                    160..365
|label= GXYGX'Y'_motif
|note= "Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342..547
/label= GXYGX'Y'_motif
/note= "Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                               523..528
/label= GXYGX'Y'_motif
/note= "Claim 1"
/label= GXYGX'Y'_motif
/note= "Claim 1"
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/label= GXYGX'Y'_motif
/note= "Claim 1"
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/note= "Claim 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               590..595
/label= GXYGX'Y'__/
/note= "Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1997.

01-DEC-1993; 159784.

01-DEC-1993; US-159784.

(HARD) HARVARD COLLEGE.

Oh SP, Olsen BR;

WPI; 97-350247/32.
                                                                                                                                                                                                                                                                                                                                             ..372
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ö Score 62; DB 24; Length 684; Pred. No. 1.34e+02; 1; Indels Mismatches Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative

213 rpgppglpg 221 윱

1 RPGPPGLQG 9 ò

Search completed: Thu Jul 30 09:33:56 1998 Job time: 20 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:36:05 1998; MasPar time 1.18 Seconds 138.599 Million cell updates/sec noular output not generated. :uo

>US-08-938-548A-12 (1-28) from US08938548A.pep 201 I RPGPPGLQGRLQRLLQANGNHAAGILIM 28

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

63816 seqs, 5850866 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 20.372; Variance 82.258; scale 0.248 a-issued 1:5\_COMB 2:PCT9\_COMB 3:backfiles Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Pred. No.	2.07e+01	2.50e+01	2.50e+01	4.40e+01	6.39e+01	6.39e + 01	6.39e+01	6.39e+01	7.69e+01	9.24e+01	9.24e+01	9.24e+01											
uo	3, Applicatio	4, Applicatio	10, Applicati	2, Applicatio	2, Applicatio	8, Applicatio	2, Applicatio	2, Applicatio	4, Applicatio	4, Applicatio	14, Applicati	4, Applicatio	14, Applicati	14, Applicati	4, Applicatio	4, Applicatio	14, Applicati		14, Applicati	6, Applicatio	25, Applicati	10, Applicati	43, Applicati
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence																
£	PCT-US91-0	PCT-US95-1	US-08-469-	US-08-494-	US-08-115-	US-08-792-	US-07-941-	PCT-US93-0	US-07-949-	US-08-017-	US-07-745-	US-08-115-	US-08-165-	US-07-921-	US-07-941-	PCT-US93-0	PCT-US94-1	us-07-688-	PCT-US91-0	PCT-US96-1	-911-10-SD	US-07-924-	US-08-062-
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Length 1	10	٠	2509	1694	199	199	199	199	199	199	296	296	296	296	296	296	296	405	405	176	26	27	27
% Query Match	32.8	32.3	32.3	30.8	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.4	28.9	28.9	28.9
Score	99	65	65	62	9	9	9	9	9	9	9	09	9	9	9	9	9	9	9	29	28	28	28
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Patent No. Patent No. Sequence 2, Sequence 2, Patent No. Patent No. Patent No. Patent No. Sequence 4, Sequence 6,	; 10 AA.	Floor Version #1.25 588
5215895-4 5215895-3 US-08-0149- US-08-017-5 5498600-2 5175255-8 5175255-8 5175255-8 5175255-8 0S-08-445- US-08-08-08-08-08-08-08-08-08-08-08-08-08-	NDARD; PRT	DECTUSS104588  1 Jeffrey 1 II.F. 1 SASS: 1 SASS: 1 Avenue, 29th Flood 1
11999 3 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	∢	Application PC/ FORMATION: 3U T: Ware, Carl F T: Ware, Carl F F SEQUENCES: 3U NEWCE ADDRESS: 3EE: C/O F1Sh 6 SEE: C/O F1Sh 6 New York New York New York New York Comp ING22-6250 READBLE FCRM: TYPE: FLOPPY d ER: IBM PC COMP ING SYSTEM: PC- FICATION DATA ATION NUMBER: PAPICATION DATA ATION NUMBER: PAPICATION DATA ATION NUMBER: PAPICATION DATA ATION NUMBER: UPART: J9910627 FICATION S30 PLICATION DATA ATION NUMBER: UPART: J9910627 FICATION NUMBER: UPART: J0 J0 NO: CAPOCKET NUMBE NUMBER: UNICATION ATION ACID GIGH AMINO ACID GIGH AMI
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,	.04588-3 ST	APPLICANT: Ware, Carl F.  APPLICANT: Browning, Jeffrey ADDRESSEE: COP Fish & Neave STREET: 875 Third Avenue, Z CITY: New YORK STRATE: New YORK COUNTRY: USA ZIP: 10022-6550 COMPUTER: READABLE FORM: WEDIUM TYPE: Floppy disk COUNTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS SOFTWARE: PATCHIN RELEASE CLASSIFICATION DATA: APPLICATION NUMBER: PCT/US9 FILING DATE: 19910627 CLASSIFICATION NUMBER: 27-794 REFRENCE/DOCKET NUMBER: B1 TELEPAN: 12-715-0600 TELEPRA: 212-715-0600 TELEPRA: 212-715-0600 TELEPRA: 14-8367 TELEPRA: 14-8367 TELERY: 10 maino acids TYPE: AMINO ACID TOPOLOGY: unknown
	FCT-US91- XXXXXX	SEGUENCE 3, A SEGUENCE 3, A PAPLICANT: TITLE OF I NUMBER OF CORRESPOND ADDRESSE STREET: CONTRY: COMPUTER REDIUM TO PERSONN SOFTWARE COMPUTER REPLICAT APPLICAT APPLICATION TELECOMMUN TELEC
	RESULT ID P XX AC X XX XX X	

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Sequence 8, Application US/08792019B
Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 60; DB 1; Length 199;
Pred. No. 6.39e+01;
3; Mismatches 0; Indels
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/792,019B FILING DATE: 03-FEB-1997
                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/115,680
                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,372
FILING DATE: 02-5EP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: INDIAUSA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
JENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                        ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 199 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                    STREET: Spring House CITY: Spring House STATE: Pennsylvania COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
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USA
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7 LQGRLQRLLQ 16
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US-08-792-019B-8
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                                                                                    Sequence 2, Application US/08494168
Patent No. 5731192
GENERAL INFORMATION:
APPLICANT: Reeders, Stephen T.
APPLICANT: 2hou, Jing
TITLE OF INVENTION: Collagen COL4A6: Gene, Protein and Method
TITLE OF INVENTION: of Detecting Collagen Deficiency
NUMBER OF SEQUENCES: 10
CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Patent No. 5437863
GENERAL INFORMATION:
APPLICANT: Williams, David A.
APPLICANT: Clark, Steven C.
TITLE OF INVENTION: Method of Treating Cell Damage or TITLE OF INVENTION: Depletion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 62; DB 1; Length lost
Pred. No. 4.40e+01;
                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION 135
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,465
FILING DATE: 27-AUG-1993
ATTORNEY/AGET INFORMATION:
NAME: SAKE, Bernhard D.
REGISTRATION NUMBER: 28,665
REGISTRATION NUMBER: 28,665
RECISTRATION NUMBER: 28,665
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 AA.
                                                                                                                                                                                                                                                        ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
JENCE 1694 AA; 165283 MW; 14956750 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20007-2109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRD FC COMPATIBLE
COMPUTER: IRD FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: PatentIn Release #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08115680
                                                         Sequence 2, Application US/08494168
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88.9%;
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Est Local Similarity 88.3°,
8; Conservative
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Sequence 14, Application US/07745382
Patent No. 5270181
GENERAL INFORMATION:
APPLICANT: McCOy, John
APPLICANT: LeVallie, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioredoxin and Thioredoxin-Like Molecules
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                             CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/017,522A
FILING DATE: 19930212
CLASSIFICATION: 530
ATTONNEY/AGENT INFORMATION:
NAME: METINER, M C
REGISTRATION NUMBER: 31,544
REFERENCE/POCKET NUMBER: 31,544
REFERENCE/POCKET NUMBER: 31,544
REFERENCE/POCKET NUMBER: 31,544
RELEPRATION NUMBER: 31,544
RELEPRANICATION INFORMATION:
TELEPRANICATION INFORMATION:
TELEPRANICATION ON: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TENGTH: 199 amino acids
TENGTH: 199 amino acids
TERPE AMINO ACID
STRANDENESS: Single
TOPOLOGY: 11near
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 29.9%; Score 60; DB 1; Length 199; Best Local Similarity 70.0%; Pred. No. 6.39e+01; Matches 7; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Cambridge CITY: Cambridge CITY: Cambridge STATE: Massachusetts COUNTRY: U.S.A.
ZIP: OL140
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
SEQUENCE 199 AA; 21429 MW; 188641 CN;
                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/07745382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
   CAMBRIDGE
   CITAL
STATE: MA.
COUNTRY: US
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 LQARLDRLLR 138
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US-07-745-382-14
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STREET: 87 CAMBRIDGEPARK DRIVE
                                                                                                                                                                                                                                                                                                                                                             COMPUTE: USA

ZIP: USA

ZIP: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATURG SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/949,516A

FILING DATE: 19-NOV-1992

CLASSIFICATION: 530

ATONREY/AGENT INPOMBATION:

NAME: Meinert, M. C.

REGISTRATION NUMBER: 31,544

REGISTRATION NUMBER: 31,544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08017522A
Patent No. 5371193
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
PAUG. STEPHAN R
APPLICANT: PAUG. STEPHAN R
APPLICANT: YANG, YU-CHUNG
TITLE OF INVENTION: A MAMMALIAN CYTOKINE, IL-11
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS - GENETICS INSTITUTE, II
                                                                                                                                              Sequence 4, Application US/07949516A
Patent No. 5700664
GENERAL INFORMATION:
APPLICANT: Yang, Yu-chung
APPLICANT: Bennett, Frances
TITLE OF INVENTION: A MAMMALIAN CYTOKINE, IL-11
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 AA.
                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
TRNCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                 ADDRESSEE: LEGAL AFFAIRS
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
                                                                                                                   Sequence 4, Application US/07949516A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08017522A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 199 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                 STANDARD;
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70.0%;
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Best Local Similarity
Matches 7; Conserv
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7 LQGRLQRLLQ 16
RESULT 9
ID US-07-949-516A-4
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US-08-017-522A-4
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Search completed: Thu Jul 30 09:36:12 1998 Job time: 7 secs.
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7 LQGRLQRLLQ 16
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                                                                                                Sequence 14, Application US/07921848
Patent No. 5292646
GENERAL INFORMATION:
APPLICANT: MCCOY, John
APPLICANT: LaVallie, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioredoxin and Thioredoxin-Like Molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 6.39e+01;
                                                                                                                                                                                                                                                                                                                SOFTWARE: PC_DOS/MS_DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,848
FILING DATE: 19920728
  296 AA
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                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
FILING DATE: 06-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,382
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                            E: Genetics Institute, Inc.
87 CambridgePark Drive
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI5188A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
FENCE 296 AA; 31769 MW; 414378 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                       STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/07941372
Patent No. 5460810
                                                                          Sequence 14, Application US/07921848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 296 amino acids
AMINO ACID
 STANDARD;
                                                                                                                                                                                      NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.9%;
70.0%;
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Matches 7; Conserv
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US-07-921-848-14
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US-07-941-372-4
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APPLICANT: Williams, David A.
APPLICANT: Williams, David A.
APPLICANT: Clark, Steven C.
TITLE OF INVENTION: Method of Treating Cell Damage or TITLE OF INVENTION: Depletion
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Howson and Howson
STREET: Spring House Corporate Center, P.O. Box 457
CITY: Spring House
STREET: Pennsylvania
COUNTRY: USA
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Pred. No. 6.39e+01;
....arrches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/941,372
FILING DATE: 19920902
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/POCKET NUMBER: INDUSI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
FENCE 296 AA; 31769 MW; 414378 CN;
                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                 ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.9%;
Similarity 70.0%;
7; Conservative
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Best Local Similarity
Matches 7; Conser
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protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 09:34:14 1998; MasPar time 4.39 Seconds 233.145 Million cell updates/sec MPsrch\_pp : oo

ular output not generated.

>US-08-938-548A-12 (1-28) from US08938548A.pep 201 1 RPGPPGLQGRLQANGNHAAGILIM 28

Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

120441 seqs, 36531193 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summarles

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d Database:

Mean 30.142; Variance 55.308; scale 0.545 Statistics:

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Pred. No.	2.25e+00	2.25e+00	6.08e+00	6.08e+00	6.08e+00	8.42e+00	8.42e+00	8.42e+00	8.42e+00	8.42e+00	8.42e+00	8.42e+00	1.16e+01	1.16e + 01	1.16e+01	1.60e+01	1.60e+01	2.20e+01	2.20e+01	2.20e+01	2.20e+01	2.20e+01	2.20e+01
Description	ő	superoxide dismutase	mALDP protein - mouse	hypothetical protein	NuMA protein - human	hypothetical protein	▭	transcription initiat	transcription initiat	transcription initiat	transcription initiat	PAS1 protein - yeast	deoxyuridine 5-tripho	hypothetical protein	RNA-directed DNA poly	adenylate cyclase (EC	fatty-acid synthase (	hypothetical protein	proteinase 3 (EC 3.4.	hypothetical protein		protein-tyrosine-phos	protein-tyrosine-phos
A	A41654	B41654	S47044	H64888	S23647	E69913	JH0496	S11712	S41307	JN0443	JN0445	A55152	D69081	S49183	S19248	A33988	G01880	S25618	PRHU3	S51155	S61858	A46101	B46101
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% Query Match Length DB	187	187	736	879	2115	178	442	442	510	525	528	1157	150	253	319	1692	2509	239	256	263	439	535	548
% Query Match	35.3	35.3	33.8	33.8	33.8	33.3	33.3	33.3	33.3	33.3	33.3	33.3			32.8	32.3	32.3		31.8	31.8	31.8	31.8	31.8
Score	7.1	71	89	89	89	29	29	29	29	67	67	29	99	99	99	65	65	64	. 64	64	64	64	64
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TESSIONS B41654
A41654
A41654
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FERENCE A41654
Fauthors Kroll, U.S.; Langford, P.R.; Loynds, B.M.
#journal J. Bacteriol. (1991) 173:7449-7457
#title Copper-zinc superoxide dismutase of Haemophilus influenzae and Haemophilus parainfluenzae.
#cross-references MuID:92041655
#accession B41654

ACCESSIONS REFERENCE #authors #journal #title

2.20e+01 2.20e+01 2.20e+01	2.20e+01 3.00e+01	3.00e+01 3.00e+01 3.00e+01	3.00e+01 3.00e+01	4.09e+01 4.09e+01 4.09e+01	4.09e+01 4.09e+01 4.09e+01	4.09e+01 4.09e+01 4.09e+01 4.09e+01
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RDYCS7 A43917 S27812	S64616 S12255 A42115	B64939 C64835 S77523	S31521 A41055 B40139	S26481 Q3YCRQ S76765	A42832 S76929 A53019	A45748 CGHU1B CGHU6B S16366
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25 25 26	25 28 28	3333	33 34 34	3 3 3 6 5 8 5 5 6 5 6 5 6 5 6 5 6 5 6 5 6 6 5 6	39 4 4 0 1 1	444 443 543

### ALIGNMENTS

RESULT

ENTRY	A41654 #type complete
OBGANTSM	
DATE	12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 20-Mar-1998
ACCESSIONS	A41654 A41654
#authors	Kroll, J.S.; Langford, P.R.; Lownds, B.M.
#journal	
#title	Copper-zinc superoxide dismutase of Haemophilus influenzae
#cross-refer	#cross-references MUID:92041655
#accession	A41654
##status	preliminary
##molecule_type	e_type DNA 1-187 ##lahel wpo
D3310D4*	foron
CLASSIFICATION	elerences ob motoriz; nin; gittoooi; rin; gittoooi  superfamily superoxide dismutase (Cu-Zn)
SUMMARY	mecaningiocein, Oxidoreducase #length 187 #molecular-weight 19536 #checksum 584
Query Match	1 35.3%; Score 71; DB 2; Length 187; Starily 35.7%; Pred No. 2.25e400.
	rvative
Db 29 KPAGP	ð
Qy 1 RPGPP	RPGPPGLQGRLLQARGNHAAGILTM 28
RESULT 2	
	B41654 #type complete
TITLE	superoxide dismutase (EC 1.15.1.1) (Cu-Zn) precursor - Haemophilus parainfluenzae
ORGANISM	#formal_name Haemophilus parainfluenzae
DATE	12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change

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Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.J.; Serror, P.; Shin, B.S.; Soldo, B.; Sorotin, A.; Tacconi, E.; Takaqi, T.; Takahashi, H.; Takemaru, K.; Takeculi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vandenbol, M.; Vannier, F.; Vassarotti, A.; Vanie, S.; Wanbutt, R.; Wander, E.; Wedler, H.; Weltzenegger, T.; Winters, P.; Wipat, A.; Yasanoto, H.; Yamane, K.; Yasumoto, K.; Tata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumsteln, E.; Yoshikawa, H.; Danchin, A. Nature (1997) 390:249-256

The complete genome sequence of the Gram-positive bacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Shiina, T.; Tanaka, K.; Takahashi, H.
#journal Gene (1991) 107:145-148
#title Sequence of hrdB, an essential gene encoding sigma-like
transcription factor of Streptomyces coelicolor A3(2):
homology to principal sigma factors.
#cross-references WUID:92077425
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#formal_name Streptomyces coelicolor
31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
24-Jul-1997
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#length 178 #molecular-weight 19609 #checksum 8831
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#length 442 #molecular-weight 48364 #checksum 4785
                                                                                                                                                                                                                                                                                                            nucleic acid sequence not shown;
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                                                                                                                                                                                                                                                                                                     preliminary; nucleic actranslation not shown
                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-178 ##label KUN ##experimental_source strain 168
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##residues 1-442 ##label SHI
##cross-references EMBL:X52983
                                                                                                                                                                                                                                                                  Bacillus subtilis.
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LQGRLQRLLQANGNHAAGIL 26
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셤 ò 

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transcription initiation factor sigma - Streptomyces griseus #formal_name Streptomyces griseus 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
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transcription initiation factor sigma katF homology
DNA binding; sigma factor; transcription initiation
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transcription initiation factor sigma katF homology
DNA binding; sigma factor; transcription initiation
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homology #label KTF
#length 442 #molecular-weight 48413 #checksum 4794
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S41306
Marcos, A.T.; Diez, B.; Gutlerrez, S.; Fernandez, F.J.;
                                                                      #formal_name Streptomyces coelicolor
03-May-1994 #sequence_revision 20-Feb-1995 #text_change
08-Sep-1997
S11712
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                                                                                                                                                                                                            Tanaka, K.; Shiina, T.; Takahashi, H. submitted to the EMBL Data Library, May 1990 Multiple homolog genes for principal sigma subunit of Streptomyces coelicolor A3(2).
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#length 510 #molecular-weight 55795 #checksum 1415
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##cross-references EMBL:X75952; NID:g440164; PID:g581664
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##cross-references EMBL:X52983; NID:g48744; PID:g48745
##experimental_source strain A3(2)
S11712 #type complete
transcription initiation factor sigma hrdB
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Pred. No. 8.42e+00;
11; Mismatches 4
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Pred. No. 8.42e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 LQEQLHSVLDTLSEREAGVVSM 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | :|: :|:: :|::| | CGRLQRLLQANGNHAAGILTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type DNA
##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            streptomyces.
S41307
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Similarity 31.8%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 33.3%;
Best Local Similarity 31.8%;
Matches 7; Conservative
                                                      coelicolor
                                                                                                                                                                                                                                                                                                                                            ##molecule_type DNA
##residues 1-44
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Matches
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Oguiza, J.A.; Martin, J.F.
submitted to the EMBL Data Library, June 1994
Three genes hrdb, had nod hrdf of Streptomyces griseus IMRU
3570, encoding sigma factor-like proteins, are
differentially expressed under specific nutritional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   into the Escherichia coli genome by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S19248 #type complete
RNA-directed DNA polymerase (EC 2.7.7.49), msDNA specific
Escherichia coli retron Ec107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                 849183 #type complete
hypothetical protein - Streptomyces griseus
#formal_name Streptomyces griseus
16-Feb-1995 #sequence_revision 12-May-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #formal_name Escherichia coli retron Ec107
20-Feb-1995 #sequence_revision 15-Oct-1996 #text_change
                  MTH1605
#length 150 #molecular-weight 16996 #checksum 5013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #checksum 1526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #molecular-weight 36363 #checksum 2019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insertion site is 82 min of E. coli K12 genetic map *superfamily reverse transcriptase nucleotidyltransferase *length 319 *molecular-weight 36363 *checksum 2015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli retron Ec107
DNA nucleotidyltransferase (RNA-directed); reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replacing a palindromic 34bp intergenic sequence tross-references MUID:92204001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 1-253 ##label MAR ##cross-references EMBL:X79980; NID:9510451; PID:9510452 ##cross-references EMBL:X79980; NID:9510451; PID:9510452 X
                                                                    Score 66; DB 2; Denyc...
Pred. No. 1.16e+01;
Transfer 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 66; DB 2; Length 253;
Pred. No. 1.16e+01;
5; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues 1-319 ##label HER
##cross-references EMBL:X62583; NID:942774; PID:942775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herzer, P.J.; Inouye, S.; Inouye, M. Mol. Microbiol. (1992) 6:345-354
Retron Ec107 is inserted into the Es
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##experimental_source E. coli wild strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##status preliminary
##molecule_type DNA
##residues 1-253 ##lab6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary
                                                                            32.8%;
                                                                                                                                                           102 GDPGFRGTLQFLLHNHGE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.8%;
Best Local Similarity 37.5%;
Matches 9; Conservative
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                                                                                                                                                                                    3 GPPGLQGRLQRLLQANGN 20
                                                                                                                        Conservative
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S49183
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S19248
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##molecule_type DNA
                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S49183
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KEYWORDS
SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #accession
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#authors
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#journal
                                                                                                                                                                                                                                                                7
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REFERENCE
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                    #gene
SUMMARY
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DATE
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GENETICS
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Gaps
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Pred. No. 1.16e+01;
4; Mismatches 5; Indels
Best Local Similarity 50.0%;
                9; Conservative
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287 ALQGRINWLLQINPEDEA 304

6 GLOGRLORLLOANGNHAA 23

Search completed: Thu Jul 30 09:34:34 1998 Job time : 20 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:34:53 1998; MasPar time 2.66 Seconds 263.713 Million cell updates/sec hlar output not generated. Run on:

>US-08-938-548A-12 (1-28) from US08938548A.pep 201 Title:

1 RPGPPGLQGRLQRLLQANGNHAAGILTM 28 Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

Searched:

69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

swiss-prot35 1:swiss1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 31.553; Variance 48.558; scale 0.650

#### SUMMARIES

Result	,	Query	:				
ò	Score	Match	Length	8	e e	Description	Pred. No.
1	71	35.3	187	Н	SODC_HAEPA	SUPEROXIDE DISMUTASE P	5.60e-01
7	71	35.3	187	Н	SODC_HAEIN	SUPEROXIDE DISMUTASE L	5.60e-01
m	69	34.3	1992	H	TR12_HUMAN	THYROID RECEPTOR INTER	1.20e+00
4	68	33.8	736	Н	ALD_MOUSE	ADRENOLEUKODYSTROPHY P	1.74e+00
ις O	68	33.8	879	Н	YDBH_ECOLI	HYPOTHETICAL 96.8 KD P	1.74e+00
9	67	33.3	79	Н	NIFU_FRAAL	NIFU PROTEIN.	2.53e+00
7	67	33.3	442	Н	HRDB_STRCO	RNA POLYMERASE PRINCIP	2.53e+00
œ	67	33.3	1157	-	PEX1_PICPA	PEROXISOME BIOSYNTHESI	2.53e+00
6	99	32.8	398	Н	VE2_HPV63	REGULATORY PROTEIN E2.	3.65e+00
10	65	32.3	307	Н	CC36_CAEEL	CUTICLE COLLAGEN 36.	5.25e+00
11	65	32.3	368	щ	COA1_POVLY	COAT PROTEIN VP1.	5.25e+00
12	65	32.3	199	Н	AFSK_STRCO	SERINE/THREONINE PROTE	5.25e+00
13	65	32.3	1692	-	CYAA_SCHPO	ADENYLATE CYCLASE (EC	5.25e+00
14	64	31.8	199	~1	IL11_MOUSE	INTERLEUKIN-11 PRECURS	7.52e+00
15	64		256	Н	PRN3_HUMAN	MYELOBLASTIN PRECURSOR	7.52e+00
16	64	31.8	624	Ч	SIR_SYNP7	SULFITE REDUCTASE (FER	7.52e+00
17	64	31.8	1477	Н	YOR1_YEAST	OLIGOMYCIN RESISTANCE	7.52e+00
18	63	31.3	255	Н	YPE1_RHORU	HYPOTHETICAL 28 KD PRO	1.07e+01
19	63	31.3	394	П	RT04_YEAST	MITOCHONDRIAL 40S RIBO	1.07e+01
20	63	31.3	702	Н	YCBY_ECOLI	HYPOTHETICAL 78.9 KD P	1.07e+01
21	63	31.3	878	-	ECR_DROME	ECDYSONE RECEPTOR (ECD	1.07e+01
22	62	30.8	256	Н	YREC_SYNP2	HYPOTHETICAL 28.7 KD P	1.52e+01
23	62	30.8	380	Н	F812_MOUSE	FACTOR VIII INTRON 22	1.52e+01

	1.52e+01	1.52e+01	1.52e+01	1.52e+01	1.52e+01	1.52e+01	1.52e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	3.03e+01	3.03e+01	3.03e+01
•	ARGININOSUCCINATE SYNT	RNA POLYMERASE SIGMA F	COLLAGEN ALPHA 1(XVIII	COLLAGEN ALPHA 6(IV) C	COLLAGEN ALPHA 4 (IV) C	COLLAGEN ALPHA 2(IV) C	PROCOLLAGEN ALPHA 2(IV	HYPOTHETICAL PROTEIN M	NEGATIVE FACTOR (F-PRO	TRANSCRIPTIONAL REGULA	HYPOTHETICAL OXIDOREDU	PULMONARY SURFACTANT-A	BETA-ARRESTIN 2.	BETA-ARRESTIN 2 (ARRES	PROTEIN UL88.	REGULATORY PROTEIN E2.	LEGUMIN PRECURSOR (BET	PHEROMONE B ALPHA 2 RE	PROBABLE DNA PACKAGING	THERMOSTABLE CARBOXYPE	COENZYME POO SYNTHESIS	COLLAGEN ALPHA 1(XI) C
	ASSY_SYNY3	RPSD_CAUCR	CA1H_HUMAN	CA64_HUMAN	CA44_HUMAN	CA24_CAEEL	CA24_ASCSU	Y652_METUA	NEF_HV2NZ	BASR_SALTY	YDGB_ECOLI	PSPA_HUMAN	ARR2_HUMAN	ARR2_BOVIN	UL88_HCMVA	VE2_HPV09	LEG1_GOSHI	BAR2_SCHCO	VTER_EBV	CTAQ_THEAQ	POOF_PSEFL	CALB_MOUSE
	Н	٦	Н	Н	Н	н	-	Н	٦	Н	٦	ч	Н	Н	ч	Н	ч	Н	Н	-	П	Н
	400	652	684	1678	1690	1758	1763	134	180	222	240	248	409	420	429	461	516	518	9	511	829	1804
	30.8	30.8	30.8	30.8	30.8	30.8	30.8	30.3	30.3	30.3	30.3	30.3	30.3	30.3	30.3	30.3	30.3	30.3	30.3	29.9	29.9	29.9
	62	62	62	62	62	62	62	61	61	61	61	61	61	61	61	61	61	61	61	9	9	9
	24	25	26	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

RESULT 1  TO SONC_HAEPA STANDARD; PRT; 16  D 2002_HAEPA STANDARD; PRT; 16  D 10-MAY-1992 (REL. 22, CREATED)  DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPID OF 01-OCT-1994 (REL. 23, LAST SEQUENCE UPID OF 01-OCT-1994 (REL. 23, LAST SEQUENCE UPID OF 01-OCT-1994 (REL. 24, LAST SEQUENCE UPID OF SUBCULLS OF PROPERTION OF SUBCULLOTES; SCOTOBACTERIP OF PROPERTY SEQUENCE FROM N.A.  RN SEQUENCE FROM N.A.  RK MOLL J.S., LANGEORD P.R., LOYNDS B.M.; RK MOLL J.S., LANGEORD P.R., LOYNDR B.M.; REDAIL HOST.  C -1 FUNCTION: MAY CONFER SURVIVAL ADVANCE OF THE HOST.  IN THE HOST.  C -1 FUNCTION: MAY CONFER SURVIVAL ADVANCE OF THE HOST.  IN THE HOST.  C -1 SUBBULLY: BELONGS TO THE CU-ZN SIDE RABL; MAGOL3; G14884;  DR RESD: POOTATS; LSDY.  DR PROSITE; PSOODAG; SOD_CU_ZN_2; 1.  ET METAL 105 105 105 COPPER (BY ST METAL 105 105 COPPER (BY ST METAL 116 114 114 114 114 114 114 114 114 114	142.  142.  143.  144.  147.
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Query Match 35.3%; Score 71; DB 1; Length 187; Best Local Similarity 35.7%; Pred. No. 5.60e-01;

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Gaps

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3; Indels Length 79;

Best Loc Matches

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-!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND THEN IS RELEASED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGMA-54 FAMILY.

EMBL; X52083; G48745; -
PIR; X1712; S11712; S11712; S1712; PROSITE; PS00715; SIGMA70_1; 1.

PROSITE; PS00716; SIGMA70_2; 1.

TRANSCRIPTION REGULATION; SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLYMERASE CORE BINDING (POTENTIAL).
H-T-H MOTIF (BY SIMILARITY).
4720321F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: TO OTHER SIGMA FACTORS THAT DO NOT BELONG TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE
       PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; FRANKIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEXI_CICPA STANDARD; PRT; 1157 AA. P46463; 01-NOV-1995 (REL. 32, CREATED) 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) PROXISOME BIOSYNTHESIS PROTEIN PASI (PEROXIN-1). PEXI OR PASI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PICHIA PASTORIS (YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 67; DB 1; L
Pred. No. 2.53e+00;
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Pred. No. 2.53e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1990 (REL: 16, CREATED)
01-NOV-1990 (REL: 16, LAST SEQUENCE UPDATE)
01-AGC-1992 (REL: 23, LAST ANNOTATION UPDATE)
RNA POLYMERASE PRINCIPAL SIGMA FACTOR HRDB.
                                                                                                                                                                                                                                                                                                                                             4CF1624F CRC32;
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                                                                                                               STRAIN-CPII;
MEDLINE; 95369734.
MEDLINE; 95369734.
GENE 161:63-67(1995).
EMBL; L129299; 6497438; -.
SEQUENCE 79 AA, 8624 MW; 4CF1624F C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGALN-53,628;
MEDLINE: 8905816.
TANAKA K., SHIINA T., TAKAHASHI H.;
SCIENCE 242:1040-1042(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 LQEQLHSVLDTLSEREAGVVSM 391
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                                                                                                                                                                                                                                                                                                                                                                                                                      33.3%;
llarity 56.3%;
Conservative
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Best Local Similarity 31.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | |:|: : ||:||||
1 RPGPPGLQGRLQRLLQ 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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422
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403 4
442 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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SEQUENCE
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       SERERES
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STRAIN=K12 / MG1655;
BLATINER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIBA H., BABA T., FUJITA K., HAVASHI K., HONJO A., HORIUCHI T.,
IKEMOTO K., INDA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H.,
KASHIMOTO K., KIM S., KIMURA S., KITAGAMA M., KITAKAWA M., MAKINO K.,
MASUDA S., MIKI T., MIZOBUCHI K., MORI H., MOTOMURA K., NAKAMURA Y.,
NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y.,
TAGAMI H., TAKENOTO K., WADA C., YAMAMOTO Y., YANO M.;
SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                              YDBH ECOLI STANDARD; PRT; 879 AA.
P52645; P77502; P76855;
D1-OCT-1996 (REL. 34, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 96.8 KD PROTEIN IN LDHA-TINA INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BUNCH P.K., MAT-JAN F., LEE N.A., DEAYALA B.A., CLARK D.P.; SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                        Score 68; DB 1; Length 736; Pred. No. 1.74e+00; 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 33.8%; Score 68; DB 1; Length 879; Best Local Similarity 45.8%; Pred. No. 1.74e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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879 AA; 96834 MW; 8BFD7CF3 CRC32;
   81858 MW; D373B00E CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32, CREATED)
32, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Mismatches
                                                                                                                                                                                                                              704 AGIPKMOGRLQELRQILGEAAAPVQPL 730
                                                                                                                                                                                                                                                                            2 PGPPGLQGRLQRLLQANGNHAAGILTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RUDD K.E.;
UNPUBLISHED OBSERVATIONS (MAR-1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U36928; -; NOT_ANNOTATED_CDS.
ECOGENE; EG13180; YDBH.
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                                                                        33.8%;
llarity 44.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-331 FROM N.A.
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P46045;
01-NOV-1995 (REL. 3
01-NOV-1995 (REL. 3
01-OCT-1996 (REL. 3
736 AA;
                                                                                                               Local Similarity
ses 12; Conser
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  SO THE SET OF SE
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SUBMITTED (JAN-1995) TO EMBL/GENBAUK/DDBJ DATA BANKS.

- FUNCTION: INVOLVED IN THE REGULATION OF SECONDARY METABOLISM BY PHOSPHORYLAATING, ON BOTH SER AND THR, THE AFSR GLOBAL REGULATORY C PROSPHORYLAATING, ON BOTH SER AND THR, THE AFSR GLOBAL REGULATORY AND PHOSPHORYLATED AT THR AND SER RESIDUES.

- I- PIM: AUTOPHOSPHORYLATED AT THR AND SER RESIDUES.

- I- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-PROTEIN KINASE.

EMBL; D15062; E120137; -

EMBL; D45382; G642157; -

RP PROSITE; PS00108; PROTEIN KINASE_ATP; 1.

R PROSITE; PS0011; PROTEIN_KINASE_LOM; 1.

R PROSITE; PS0011; PROTEIN_KINASE_LOM; 1.
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-I- CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.

-I- IN CONTRAST TO YEAST CYCLASE, S.POMBE CYCLASE IS NOT LIKELY TO BE REGULATED BY RAS PROTEINS.

-I- SIMILARITY: THE REPEATED LEUCINE-RICH (LRR) SEGMENT IS FOUND IN MANY PROTEINS. NUMBER IN THIS PROTEIN: 22.

-I- SIMILARITY: BELONGS TO CLASS-3 OF ADENYLYL CYCLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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-!- FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL
                                                                                                                                                                                      STRAIN-A3(2);
MEDLINE; 94341568.
MATSUMOTO A., HONG S.K., ISHIZUKA H., HORINOUCHI S., BEPPU T.;
GENE 146:47-56(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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MEDLINE; 90046723.
YOUNG D., RIGGS M., FIELD J., VOJTEK A., BROEK D., WIGLER M.;
PRROC. NAIL. ACAD. SCI. U.S.A. 86:7989-7993(1989).
                                                                                                          PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 65; DB 1; Length 799;
Pred. No. 5.25e+00;
7; Mismatches 8; Indels
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
SERINE/THREONINE PROTEIN KINASE AFSK (EC 2.7.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 PPGPPGLQGRLQRLLQANGNHAAG 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83781 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 32.3%;
Best Local Similarity 37.5%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                              STREPTOMYCES COELICOLOR
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44
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                                                                                                                                                             SEQUENCE FROM N.A.
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P14605;
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SEQUENCE
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BINDING
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 97070356.
MEDLINE; 97070356.
MEDLINE; 97070356.
MORRIS J.C., FINNERTY H., BENNET F., TURNER K.J., WOOD C.R.;
EXP. HEMATOL. 24:1369-1376(1996).
-i- FUNCTION: THIS PROFIZEN STIMULATES PLASMACYTOMA PROLIFERATION,
T-CELL-DEPENDENT DEVELOPMENT OF IMMUNOGLOBULIN-PRODUCING B
CELLS AND SYMERGIZES WITH IL-3 IN SUPPORTING MURINE
MEGAKARYOCYTE COLONY FORMATION (BY SIMILARITY).
EMBL; 003421; 6415654;
MGD; MGI:107613; IL11:
CYTOKLINE; GROWTH FACTOR; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 199;
                                                                                       SYNTHESIS; MAGNESIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                       EUCINE-RICH REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW; 20E7D7D8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 64; DB 1; L. Pred. No. 7.52e+00; 4; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 65; DB 1; L
Pred. No. 5.25e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERLEUKIN-11.
1CB30772 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
INTERLEUKIN-11 PRECURSOR (IL-11).
-1- SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN. EMBL; M2699; G173339; -. EMBL; M24942; G173379; -. PIR; A33988; A33589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PP2C-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                       CAMP
                                                                                                                                                                                     ER
RR
                                                                                                                                                                                                                                               LRR
                                                                                                                                                                                                                                  LRR
                                                                                       REPEAT; LEUCINE-REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21522 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.8%;
larity 53.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1539 PVQLQGRLERLIKS 1552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 PPGLOGRLORLLOA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
199 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LT 14
IL11_MOUSE
P47873;
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:35:23 1998; MasPar time 5.13 Seconds 230.058 Million cell updates/sec Jular output not generated. : 0

>US-08-938-548A-12 (1-28) from USO8938548A.pep 201 1 RPGPPGLQGRLQANGNHAAGILTM 28 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

140542 seqs, 42109429 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl5
1:sp\_fungi 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_huhe 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Mean 30.024; Variance 52.279; scale 0.574 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	2.55e-01	3.68e-01	7.59e-01	3.12e+00	4.42e+00	6.22e+00	6.22e+00	6.22e+00	6.22e+00	6.22e+00	6.22e+00	6.22e+00	6.22e+00	6.22e+00	8.74e+00	8.74e+00	8.74e+00	8.74e+00	8.74e+00	8.74e+00
Description	TIGHT JUNCTION PROTEIN	PAR INTERACTING PROTEI	K+ CHANNEL BETA4 SUBUN	LEUCINE ZIPPER WITH BA	NUMA PROTEIN.	YONC PROTEIN.	MAXP1.	RNA POLYMERASE SIGMA F	ARTICULIN P60.	DNA POLYMERASE III TAU	HRPG.	DEOXYCYTIDINE-TRIPHOSP	UNKNOWN GENE.	T24D5.1.	RNA-DIRECTED DNA POLYM	THYROID HORMONE INDUCE				
QI	095168	035821	P97382	091640	014980	031955	035141	P95644	059913	P77951	059813	059814	927212	045998	060245	027642	054224	922732	005804	091654
DB	4	2	10	12	~	σ	10	σ	σ	σ	σ	σ	ო	σ	σ	ά	σ	m	σ	12
% Query Match Length DB	1174	1277	249	331	2115	178	413	462	510	514	525	528	568	608	130	150	253	304	319	335
Query Match	37.8	37.3	36.3	34.3	33.8	33.3	33.3	33.3	33.3	33.3	33.3	33.3	33.3	33.3	32.8	32.8	32.8	32.8	32.8	32.8
Score	92	75	73	69	68	67	. 67	67	67	29	67	. 67	67	67	99	99	99	99	99	99
Result No.	-	73	m	4	S	9	7	۵	σ	10	11	12	13	14	15	16	. 17	18	19	20

8.74e+00 8.74e+00	8.74e+00	1.22e+01	1.22e+01	1.22e+01	1.71e+01	1.71e+01	1.71e+01	1.71e+01	1.71e+01	1.71e+01	1.71e+01	1.71e+01	2.37e+01	2.37e+01	2.37e+01	2.37e+01	2.37e+01	2.37e+01	2.37e+01	2.37e+01	3.29e+01	3.29e+01
HYPOTHETICAL 41.3 KD P CARA.	H06001.2. PRISTINAMYCIN I SYNTHA	RETINOID X RECEPTOR IN	P160 MYB-BINDING PROTE	FATIY ACID SYNTHASE (E	PUTATIVE SIGMA-54 DEPE	ORF263.	HOMODA HYDROLASE.	ORF328 (FRAGMENT).	HRPE.	PROTEIN-TYROSINE PHOSP	KM-102-DERIVED REDUCTA	PUTATIVE EPIDERMAL CEL	FROM BASES 1860594 TO	NODO.	HYPOTHETICAL 85.5 KD P	EXTRACELLULAR MATRIX P	KIAA0310.	POLYPROTEIN.	TYLACTONE SYNTHASE MOD	POLYKETIDE SYNTHASE MO	C-SRC TYROSINE KINASE.	A TYPE IV COLLAGEN (FR
Q09636 Q50983	017909	060811	035851	016702	050872	931722	051980	053921	052495	027932	099475	204164	P76237	007309	P73339	006452	015027	P89521	033958	030766	091952	Q12823
ოთ	mσ	12	10	~	σ	ø	σ	σ	σ	m	~	m	σ	σ	σ	m	~	디	σ	σ	12	7
365	1465	580	1344	2509	140	263	288	294	439	548	549	1348	556	633	770	812	881	972	1841	3654	527	1690
32.8	32.8	32.3	32.3	32.3	31.8	31.8	31.8	31.8	31.8	31.8	31.8	31.8	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	30.8	30.8
99	9 9	65	65	9	64	64	64	64	64	64	64	64	63	63	63	63	63	63	63	63	62	62
22	23 24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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·			0;
LT 1 095168 09168 09166 09166 09166 10-FEB-1997 (TREMBLREL. 02, CREATED) 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE) 101-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE) 20-SONTION PROFEIN. 20-CANTS FAMILIARIS (DOG). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	EUTHERIA; CARNIVORA. [1] SEQUENCE FROM N.A. MEDLINE; 94179414. J. CELL BIOL. 124:949-961(1994).	SEQUENCE FROM N.A. MEDILINE; 96421547. BERATCH M., JESAITIS L.A., GALLIN W., GOODENOUGH D.A., STEVENSON B.R.; J. BIOL. CHEM. 271:25723-25726(1996). SEQUENCE FROM N.A. GOODENOUGH D.A.; SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.	SEQUENCE FROM N.A.  BEATCH M.; SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.  EMBL; L271122, G1536970;  SEQUENCE 1174 AA; 132085 MW; 2FA16B83 CRC32;  QUELY MAICH  37.8%; SCOIE 76; DB 4; Length 1174;  Best Local Similarity 32.1%; Pred. No. 2.55e-01;  Matches 9; Conservative 12; Mismatches 7; Indels 0
RESULT ID OD DT OD DT OD DE T	S R R R R R R	R R R R R R R R R R R R R R R R R R R	RA RA RI DR SQ Qu Ma

268 RSPSPELRGRPDHAGOPDSDRPIGVLLM 295 |::||:||:||: | RPGPPGLQGRLQRLGANGNHAAGILTM 28

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RESULT 2 ID 035821

PRT; 1277 AA. PRELIMINARY;

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EMBL;
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                                                                                                                                                                                                                                                                                                         Matches
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          SYMMAN
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MASUDA S., MAUEL C., MEDIGUE C., MEDINA N., MELLADO R.P., MIZUNO M.,
MOESTL D., NAKAI S., NOBACK M., NOONE D., O'REILLY M., OGRAR K.,
A OGIWARA A., OUDGGA B., PARK S.H., PARRO V., POHL. T.M., PORTETELLE D.,
RAPOPORT G., REY M., REYNOLDS S., RIEGER M., RIVOLTA C., ROCHA E.,
RAPOPORT G., REY M., SADAIE Y., SATO T., SCAMLAN E., SCHENELE B.,
A SCHROETER R., SCOFFONE F., SETGIGHIA I., SHKOWSKA A., SEROR S.J.,
A SCHROETER R., SCOFFONE F., SETGIGHIA I., SHKOWSKA A., SEROR S.J.,
A TAKARABHI H., TAKEMARU K., TAKEGGHI M., TAMAKOSHI A., TAKARABI T.,
A TAKARABHI H., TAKEMARU K., TAKEGGHI M., TAMAKOSHI A., TANAKA
A VANNIER F., VASSAROTTI A., TAKEGHI M., TAMAKOSHI A., TANAKA
A WANIER F., VASSAROTTI A., VIARI A., WAMBUTT R., WEDLER H.,
A PASUMOTO K., YATA K., YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E.,
A YOSHIKAWA H., DANCHIN A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RATTUS NORVEGICUS (RAI).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Pred. No. 6.22e+00;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; 299115; E1183561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SLEPNEV V.I., DE CAMILLI P.V.;
SUENHITUED (C.1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, AF0012251; G2459833; -.
SEQUENCE 413 Aa; 46679 MW; 69A87FCC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAINS-ATCG3209;
STRAIL A., CONCHA M.I., FIGUEROA J., LEON G.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUBACTERIA; FIRMICUTES; ACTINOMYCETES; RENIBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAY-1997 (TREMBLREL. 03, CREATED)
01-WAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.3%; Score 67; DB 9; L
larity 45.0%; Pred. No. 6.22e+00;
Conservative 4; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA7B8ED0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      413 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      462 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19609 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MATRLQKALTEVGNHTTGNL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : |||: | |||:| |
7 LOGRLQRLLQANGNHAAGIL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05,
05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.3%;
Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA POLYMERASE SIGMA FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RENIBACTERIUM SALMONINARUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              035141 PRELIMINAR
035141,
01-JAN-1998 (TREMBLREL: 0)
01-JAN-1998 (TREMBLREL: 0)
01-JAN-1998 (TREMBLREL: 0)
                                                                                                                                                                                                                                                                                                                                                          NATURE 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 RPVRPGLQQRLRR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || || |||| ||:|
| RPGPPGLQGRLQR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P95644
P95644;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAXP1
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-1- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND THEN IS RELEASED.

EMBL: X75922; G581664; -.

PROSITE; PSO0715; SIGMA70_1; 1.

PROSITE; PSO0716; SIGMA70_2; 1.

TRANSCRIPTION REGULATION; SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND THEN IS RELEASED.
                                                                                             EMBL; Y10835; E294130; -.
PROSITE; PS00715; SIGMA70_1; 1.
PROSITE; PS00716; SIGMA70_2; 1.
TRANSCRIPTION REGULATION; SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ., DIEZ B., GUTIERREZ S., FERNANDEZ F.J., OGUIZA J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREPTOMYCES GRISEUS.
PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREPTOMYCES GRISEUS.
PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE
                                                                                                                                                                                                                                                                                                                                   Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 510;
                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TREMBLREL. 02, CREATED)
(TREMBLREL. 02, LAST SEQUENCE UPDATE)
(TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                         Score 67; DB 9; L/
Pred. No. 6.22e+00;
11; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 67; DB 9; L
Pred. No. 6.22e+00;
                                                                                                                                                                                                                                                                    462 AA; 50504 MW; E54BBFE5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    510 AA; 55795 MW; C3CB64EB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         510 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 514 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 LQEQLHSVLDTLSEREAGVVAM 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  438 LQEQLHSVLDTLSEREAGVVSM 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.3%;
llarity 31.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA POLYMERASE SIGMA FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA POLYMERASE SIGMA FACTOR
                                                                                                                                                                                                                                                                                                                            33.3%;
imilarity 31.8%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THEN IS RELEASED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1997 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=IMRU 3570;
MEDLINE; 95189101
MARCOS A.T., DIEZ
                                                                                                                                                                                                                                  DNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1997
01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MARTIN J.F
                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
1D 059913
1D 059913
1D 01-NOV-11
1D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 10
P77951
P77951;
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GN HRPG.
OS PSEUDOMONAS SYRINGAE.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC PSEUDOMONADACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-61;
RX MEDLINE; 96025090.
RA HUNG H.C., LIN R.H., CHANG C.J., COLLMER A., DENG W.L.;
RL MOL. PLANT MICROBE INTERACT. 8:733-746(1995).
DR EMBL, 022813; G818900; -.
SQ SEQUENCE 130 AA; 13950 MW; 5CDEACF8 CRC32;
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Query Match 32.8%; Score 66; DB 9; Length 130;
Best Local Similarity 40.7%; Pred. No. 8.74e+00;
Matches 11; Conservative 8; Mismatches 7; Indels 1; Gaps 1;
Db 80 PGPCGLADLLNRL-ESLANQRAALLSL 105

80 PGPCGLADILINRL-ESLANGRAALLSI 105 ||| || || || || :::|:|:: 2 PGPPGLQGRLQALLQANGNHAAGILIM 28 Search completed: Thu Jul 30 09:35:47 1998 Job time: 24 secs.

****	(TM)
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:27:56 1998; MasPar time 8.78 Seconds 589.674 Million cell updates/sec pular output not generated. Run on:

>US-08-938-548a.10 (1-123) from USO8938548a.pep 899 1 VPWAAVTLLLLLLPPALLS......GRGCPTVTTALAPRGGSGV 123

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

Searched:

140542 seqs, 42109429 residues

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl5
1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Mean 39.425; Variance 86.061; scale 0.458 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	No.	Score	% Query Match	% Query Match Length DB	DB	A	Description	Pred. No.
•	П	106	11.8	629	. 8	023352	HYPOTHETICAL 74.6 KD P	2.41e-02
	~	103	11.5	567	10	008770	PLATELET GLYCOPROTEIN	5.93e-02
	ო	86	10.9	641	10	008463	FRIZZLED PROTEIN HOMOL	2.57e-01
	4	94	10.5	574	10	035298	ACYLOXYACYL HYDROLASE.	8.09e-01
	S	93	10.3	331	15	091640	LEUCINE ZIPPER WITH BA	1.07e+00
	ø	93	10.3	1174	7	095168	TIGHT JUNCTION PROTEIN	1.07e+00
	7	92	10.2	106	ω	041051	PROLINE- AND LEUCINE-R	1.42e+00
	œ	91	10.1	602	10	063921	CYCLOOXYGENASE ISOFORM	1.87e+00
	σ	91	10.1	602	2	063684	CYCLOOXYGENASE 1.	1.87e+00
	10	90	10.0		~	099523	SORTILIN PRECURSOR.	2.47e+00
	11	88	6.6		2	062731	PROSTAGLANDIN H SYNTHA	3.25e+00
	12	88	9.8	226	თ	006319	HYPOTHETICAL 23.1 KD P	4.27e+00
	13	88	8.6	335	12	091654	THYROID HORMONE INDUCE	4.27e+00
	14	87	9.7	252	σ	005582	HYPOTHETICAL 25.9 KD P	5.60e+00
	15	87	9.7	583	12	090491	DNA BINDING PROTEIN E1	5.60e+00
	16	87	9.7	599	~	015122	PROSTAGLANDIN ENDOPERO	5.60e+00
	17	87	9.7	1238	'n	018780	SIMILARITY TO MOUSE SM	5.60e+00
	18	98	9.6	410	σ	P72841	HYPOTHETICAL 48.1 KD P	7.32e+00
	19	98	9.6	1099	2	P97527	NB-2.	7.32e+00
	20	82	9.5	363	7	002839	PORCINE MEMBRANE COFAC	9.56e+00

RESULT 2 PRELIMINARY; PRT; 567 AA. 10 008770 AC 00710; CREMBLREL. 04, CREATED) DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE) DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)

9.56e+00 1.25e+01 1.25e+01 1.25e+01	1.25e+01 1.25e+01 1.25e+01 1.62e+01 1.62e+01 1.62e+01	1.62e+01 1.62e+01 1.62e+01 1.62e+01 1.62e+01	2.10e+01 2.10e+01 2.10e+01 2.10e+01 2.10e+01	2.72e+01 2.72e+01 2.72e+01 2.72e+01 2.72e+01
RNA POL ER ISOFO RECURSOR 30.9 KD	HYPOTHETICAL 72.6 KD P ANION EXCHANGER 2 A (F DIACYLGLYCEROL KINASE 3' ORF. NEUROVIRULENCE FACTOR. MYOMODULIN (FRAGMENT).	ECURS ESTER PROTE LASE	HYPOTHETICAL 27.7 KD P MYOMODULIN NEUROPEPTID FROM BASES 1860594 TO VERY LARGE TEGIMENT PR TYLACTONE SYNTHASE MOD	FERRIC ENTEROBACTIN TR FROM BASES 2573751 TO F18A12.4 PROTEIN. GUANYLATE CYCLASE ISOF MYOSIN.
Q83101 Q60471 Q43495 Q33285	065568 060470 000542 061639 012396	007974 035849 017021 P72405 019179	P95156 Q25413 P76237 P89459 O33956	Q46729 P76559 O16791 O02809 Q39160
11086	12°21°	E 0 E 0 4	9 2 4 4 9	<b>ω</b> ω ω 4 ∞
878 84 102 277	701 729 1117 147 248 329	370 440 498 551 1109	264 350 3122 3729	40 347 734 1110 1520
00000 00000	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	00000
88 8 8 8 8 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		22222 88888	81 81 81 81
223 243 243 243	3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	33 3 3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5	337 338 409	4 4 4 4 4 1 4 6 4 6 7

### ALIGNMENTS

RESULT 1 ID 023352 PRELIMINARY; PRT; 679 AA. AC 023352:		RN 11) RP SEQUENCE FROM N.A. RA BEVAN M., STIEKEMA W., MURPHY G., WAMBUTT R., POHL T., TERRYN N., RA KREIS M., KAVANAGH T., ENTIAN K.D., RIEGER M., JAMES R., RA PUIGDOMENECH P., HATZOPOULOS P., OBERRAIER B., DUESTERHOFT A., JONES RA PALME K., ANGORGE W., DELSENY M., BANCROFT I., MEWES H.W., SCHUELLER PA CHAIMADATIC N.	Query Match 11.8%; Score 106; DB 8; Length 679; Best Local Similarity 32.3%; Pred. No. 2.41e-02; Matches 20; Conservative 16; Mismatches 22; Indels 4;	Db 598 KYCRSK-YETIHGQNHDNAADVLELAIKREMPAELL-R-ASLRHTNEDGRNFLLNVGRSA       :     :     :	Db 655 SP 656 : : Ov 94 GA 95
	ONEAE;	TERRYN N., OFT A., JONES J., W., SCHUELLER.C.,		NFLLNVGRSA 654 :  :     AGILTMGRRA 93	

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Gaps

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RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                       MEDLINE; 94099619.
FENG L., SUN W., XIA Y., TANG W.W., CHANMUGAM P., SOYOOLA E., WILSON C.B., HANNG D., ACH. BIOCHEM. BIOPHYS. 307:361-368(1993).
EMBL; S67721; G460556; -.
NOM_TER 602 602
SEQUENCE 602 AA; 69158 MW; 4EBDC921 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-FISHER 344;
FENG L., SIN W., XIA Y., TANG W.W., CHANMUGAM P., SOYOOLA E.,
WILSON C.B., HWANG D.;
ARCH. BIOCHEM. BIOPHYS. 307:0-0(0).
EMBL; U03388; G415638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOMMERUP N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PETERSEN C.M., NIELSEN M.S., JACOBSEN L., TOMMERUP N. ROIGARD H., GLIEMANN J., MADSEN P., MOESTRUP S.K.; SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; X98488; E246784; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
CYCLOOXYGENASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 90; DB 2; Le
Pred. No. 2.47e+00;
5; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                   Score 91; DB 10; Pred. No. 1.87e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 91; DB 10; Pred. No. 1.87e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SORTILIN.
D2E351B9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             602 AA; 69115 MW; DC2236E9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             833 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 LLLLLLLPPA--LLS-LGVDAQPLPDCC 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 LLLLLLPPPPVLLTDAGVPSPVIP-CC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 LILLLLPPPPVLLTDAGVPSPVIP-CC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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92408 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03,
03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.1%;
Best Local Similarity 57.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.1%;
Best Local Similarity 57.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.0%;
Best Local Similarity 53.3%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 10
099523 PRELIMINAR
099523, 099523,
01-MAY-1997 (TREMBLREL. 0
01-MAY-1997 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33
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833 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SORTILIN PRECURSOR.
       EUTHERIA; RODENTIA
                                                                         SEQUENCE FROM N.A. MEDLINE; 94099619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLT 9
Q63684
Q63684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
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01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
PROLINE- AND LEUCINE-RICH PROTEIN.
PISUM SATIYUM (GARDEN PEA).
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE; FABALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : |: :| |:|| :: |:::::: |:::::: | |::| | |::| | |::| |::| |::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 RSRSPSPELRGRPDHAGQPDSDRPIGVLLMKSKANEEYGLRLGSQIFIKQMTRTALATKD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
CYCLOOXYGENASE ISOFORM COX-1 (FRAGMENT).
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; CARNIVORA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 93; DB 4; Length 1174; Pred. No. 1.07e+00; 18; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.2%; Score 92; DB 8; Length 106; Best Local Similarity 61.9%; Pred. No. 1.42e+00; Matches 13; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RODRIGUEZ-CONCEPCION M., PEREZ-GARCIA A., BELFRAN J.;
SUBMITIED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; 267873; E208986; -
SEQUENCE 106 AA; 11828 MM; A45AD924 CRC32;
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 96421547.
BEATLIS L.A., GALLIN W., GOODENOUGH D.A.,
STEVENSON B.R.;
J. BIOL. CHEM. 271:25723-25726(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BEATCH M.;
SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; L27152; G1536970; -.
SEQUENCE 1174 AA; 132085 WW; 2FA16B83 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOODENOUGH D.A.;
SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          602 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q41051 PRELIMINARY; PRI; Q41051; 01-NOV-1996 (TREMBLREL. 01, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                           SEQUENCE FROM N.A.
MEDLINE, 94179414.
JESATIES L.A., GODENOUGH D.A.;
J. CELL BIOL. 124:949-961(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 ILLLLLPPPLLLLLMRPLPL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.3%;
29.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 29.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:
120 GS 121
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                                 119 PTGLQGNMAAV-SAEGN-GNRFVVIAVETSQPL-PAPSPGKDCSKVTFSGTQLRGGIEV 174
                                                                                                                                                                                                    01-NOV-1996 (TREMBLEEL. 01, LAST ANNOTATION UPDATE)
DNA BINDING PROTEIN E12.
BRACHYDANIO RERIO (ZEBRALEH) (ZEBRA DANIO).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
 15; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                     MEDLINE; 95001558.
WHELLINE; 95001558.
WHELLECK C., FROMENTAL-RAMAIN C., CAMPOS-ORIEGA J.A.;
WECH. Dev. 46:73-85(1994).
EMBL; X76997; G509754; -.
                                                                                                                                                                     01, CREATED)
01, LAST SEQUENCE UPDATE)
01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                               583 AA; 62625 MW; A874D9E2 CRC32;
                                                                                                                                     583 AA
                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A. TRAIN-WT; TISSUE-WHOLE EMBRYO;
                                                                                                                                     PRELIMINARY;
19; Conservative
                                                                                                                                                                       (TREMBLREL. (TREMBLREL. (TREMBLREL. (
Matches
                                                                                                                  RESULT
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Gaps

Score 87; DB 12; Length 583; Pred. No. 5.60e+00; 10; Mismatches 15; Indels

Query Match 9.7%; Best Local Similarity 38.6%; Matches 17; Conservative g

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Search completed: Thu Jul 30 09:28:17 1998 Job time: 21 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:27:25 1998; MasPar time 5.12 Seconds 602.279 Million cell updates/sec Run on:

pular output not generated.

>US-08-938-548A-10 (1-123) from US08938548A.pep 899 1 VPWAAVTLILLLLLPPALLS.......GRGCPTVTTTALAPRGGSGV 123 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

69111 seqs, 25083644 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot35 1:swissl

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 41.408; Variance 75.349; scale 0.550

#### SUMMARIES

	Pred. No.	1.48e-02	7.91e-02	7.91e-02	7.91e-02	7.91e-02	3.99e-01	7.51e-01	1.03e+00	1.03e+00	1.90e+00	1.90e+00	1.90e+00	1.90e+00	2.57e+00	2.57e+00	2.57e+00	2.57e+00	3.48e+00	3.48e+00	3.48e+00	3.48e+00	3.48e+00	3.48e+00
	Description	SECRETIN PRECURSOR (FR	FIBULIN-1, ISOFORM A P	FIBULIN-1, ISOFORM B P	FIBULIN-1, ISOFORM C P	FIBULIN-1, ISOFORM D P	PHOSPHATIDYLCHOLINE-ST	ATRIAL NATRIURETIC PEP	4-1BB LIGAND (4-1BBL).	PHOSPHATIDYLCHOLINE-ST	HYPOTHETICAL PROTEIN H	PHOSPHATIDYLCHOLINE-ST	SEC14 CYTOSOLIC FACTOR	COMPLEMENT C3 PRECURSO	PLACENTAL LACTOGEN I P	LIPASE 1 PRECURSOR (EC	FERRIC ENTEROBACTIN IR	FIBRIL-FORMING COLLAGE	E PROTEIN.	LYSIS PROTEIN.	EPHRIN-A3 PRECURSOR (E	COMPLEMENT C1Q SUBCOMP	LIPASE 3 PRECURSOR (EC	HYPOTHETICAL 36.0 KD P
	Ð	SECR_PIG	FBLA_HUMAN	FBLB_HUMAN	FBLC_HUMAN	FBLD_HUMAN	LCAT_HUMAN	ANPA_HUMAN	41BL_HUMAN	LCAT_MOUSE	YCEC_HAEIN	LCAT_PAPAN	SC14_YARLI	CO3_RAT	PLC1_BOVIN	LIP1_PSYIM	FEPD_ECOLI	CAFF_RIFPA	VGE_BPS13	VGE_BPPHX	EFA3_HUMAN	C1QB_HUMAN	LIP3_MORSP	YCEC_ECOLI
	DB	н	-	Н	Н		1	Н		-	-	Н	Н	Н	Н	н		Н	1	~	-	-	-4	~
	Query Match Length DB	131	266	109	683	703	440	1061	254	438	322	440	497	1663	236	317	334	1027	90	90	238	251	315	319
ф	Query	11.2	10.7	10.7	10.7	10.7	10.1	9.0	9.8	9.8	9.6	9.6	9.6	9.6	9.5	9.5	9.5	9.5	9.3	9.3	9.3	9.3	9.3	6.9
	Score	101	96	96	96	96	91	89	88	88	86	86	86	86	85	82	82	82	84	84	84	84	84	84
	Result No.		7	m	4	5	9	7	ω	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

3.48e+00	3.48e+00	3.48e+00	3.48e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	6.30e+00	6.30e+00	6.30e+00
GTPASE ACTIVATING PROT	LUTROPIN-CHORIOGONADOT	PROTEIN-TYROSINE PHOSP	TALIN.	PLATELET GLYCOPROTEIN	OXALATE OXIDASE PRECUR	SL CYTOKINE PRECURSOR	INFECTED CELL PROTEIN	INFECTED CELL PROTEIN	INFECTED CELL PROTEIN	PHOSPHATIDYLCHOLINE-ST	PHOSPHATIDYLCHOLINE-ST	HYPOTHETICAL 59.6 KD P	SERUM ALBUMIN PRECURSO	CELL DIVISION PROTEIN	TRANS-ACTING TRANSCRIP	TRANS-ACTING TRANSCRIP	PROTEIN-TYROSINE PHOSP	ANGIOTENSIN-CONVERTING	INFECTED CELL PROTEIN	METALLO-BETA-LACTAMASE	ADENYLATE CYCLASE, TYP
RN_DROME	LSHR_PIG	PIPX MOUSE	TALI_MOUSE	GPBB_PAPCY	OXO2_HORVU	FL3L_HUMAN	ICP3_HSV11	ICP3_HSV1D	ICP3_HSV1F	LCAT_RABIT	LCAT_RAT	YABK_ECOLI	ALBU_CHICK	FTSH_PORPU	ICPO_HSVBJ	ICPO_HSVBK	PTPX_RAT	ACE_RABIT	ICP3_HSV1N	BLA1_XANMA	CYA6_MOUSE
н	н	Н	Н	Н	Н	ч	Н	-1	н	Н	н	H	Н	Н	Н	Н	-1	Н	~4	н	-
384	969	1001	2541	208	224	235	248	252	263	440	440	536	615	628	9/9	9/9	1004	1310	245	290	1165
9.3	9.3	9.3	9.3	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.1	9.1	9.1
84	84	84	84	83	83	83	83	83	83	83	83	83	83	83	83	83	83	83	82	82	85
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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REDUENCE OF 30-44.

REDUENCE OF 30-44.

REDUENCE SEQUENCE OF 30-44.

REDUENCE SECULAR SECULAR SECULAR MATRIX.

CELL, 58:623-629(1989).

-i-SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.

CELL, 58:623-629(1989).

CELL, 58:623-62(1989).

CELL, 58:68-62(1989).

CEL
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EUTHERIA; PRIMATES.
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Pred. No. 7.91e-02;
3; Mismatches 8; Indels
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3 X ANAPHYLATOXIN REPEATS
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MEDALINE; 91100426.
ARGENS W.S., TRAN H., BURGESS W.H., DICKERSON K.;
J. CELL BIOL. 111:3155-3164(1990).
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-> SH (IN REF. 2)
3A6E492B CRC32;
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01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FIBULIN-1, ISOFORM C PRECURSOR.
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Best Local Similarity 57.1%;
Matches 16; Conservative
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3 X ANAPHYLATOXIN REPEATS.
ANAPHYLATOXIN-LIKE 1.
ANAPHYLATOXIN-LIKE 1.
ANAPHYLATOXIN-LIKE 2.
CALLIKE 1.
EGF-LIKE 2, CALCIDW-BINDING (POTENTIAL).
EGF-LIKE 3, CALCIDW-BINDING (POTENTIAL).
EGF-LIKE 6, CALCIDW-BINDING (POTENTIAL).
EGF-LIKE 7, CALCIDW-BINDING (POTENTIAL).
EGF-LIKE 7, CALCIDW-BINDING (POTENTIAL).
EGF-LIKE 7, CALCIDW-BINDING (POTENTIAL).
EGF-LIKE 9, CALCIDW-BINDING (POTENTIAL).
EGF-LIKE 7, CALCIDW-BINDING (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 89354537.

ARGRAVES W.S., DICKERSON K., BURGESS W.H., RUOSLAHTI E.;

ARGRAVES W.S., DICKERSON K., BURGESS W.H., RUOSLAHTI E.;

CELL 58:623-629(1989).

-! ALTERNATIVE PRODUCTS: FOUR FORMS OF FIBULIN-1; A (AC P23142), B

(SHOWN HERE), C (AC P23144) AND D (AC P37889); DIFFERING ONLY IN

THEIR C-TERMINAL REGIONS, ARE PRODUCED BY ALTERNATIVE SPLICING.
-! SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.
-! SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.
-! SIMILARITY: CONTAINS 9 PGF-LIKE DOMAINS.
-! SIMILARITY: CONTAINS 9 PGF-LIKE DOMAINS.
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PROSITE: PS00010;
PROSITE: PS00022; EGF_1; FALSE_NEG.
PROSITE: PS01177; ANAPHYLATOXIN_1; 3.
PROSITE: PS01178; ANAPHYLATOXIN_2; 3.
PROSITE: PS01186; EGF_2; 3.
PROSITE; PS01187; EGF_2; 8.
SIGNAL; ALTERNATIVE SPLICING; GLYCOPROTEIN; EXTRACELLULAR MATRIX;
REPEAT; PLASMA; EGF_1IKE DOMAIN; CALCIUM-BINDING.
                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDILINE; 91100424 91100424 ARBALVES W.S., TRAN H., BURGESS W.H., DICKERSON J. CELL BIOL. 111:3155-3164(1990).
                              01-NOV-1991 (REL. 20, CREATED)
01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FIBULIN-1, ISOFORM B PRECURSOR.
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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VARIANT LYS-276.
MEDLINE; 92387377.
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MEDLINE; 96400966.
  VARIANT ARG-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THIS ENZYME
                                                                                                                                                                     VARIANT ILE-317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISEASES
                                                                                                                                                                                                                                                                                ASSMANN G.;
                                                                                                                                                                                                 KASUGA M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASSMANN G.
  ï
                                                            Gaps
                                                                                                                                                                                                                                                                                        B., KOHR W.,
                                                                                                                                                        20-MAR-1987 (REL. 04, CREATED)
20-MAR-1987 (REL. 04, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LEST SEQUENCE UPDATE)
PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
(LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 92147865.
KLEIN H.-G., LOHSE P., PRITCHARD P.H., BOJANOVSKI D., SCHMIDT H.,
BREWER H.B. JR.;
J. CLIN. INVEST. 89:499-506(1992).
[9]
                                                                                                                                                                                                                                                                                                                                                                                                  M.D.,
                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARTIAL SEQUENCE, AND DISULFIDE BONDS.
MEDLINE; 87137578.
YANG C., MANOOGIAN D., PAO Q., LEE F., KNAPP R.D., GOTTO A.M.
POWNALL H.J.;
J. BIOL. CHEM. 262:3086-3091(1987).
                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                 G.D., WATERFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROGNE S., SKRETTING G., LARSEN F., MYKLEBOST O., MEVAG B., CARLSON L.A., HOLMQUIST L., GJONE E., PRYDZ H.; BIOCHEM. BIOPHYS. RES. COMMUN. 148:161-169(1987).
                                     Score 96; DB 1; Length 703;
Pred. No. 7.91e-02;
3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCHINDLER P.A., SETTINERI C.A., COLLET X., FIELDING C.J.,
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 86205950.
MCLEAN J., FIELDING C., DRAYNA D., DIEPLINGER H., BAER
HENZEL W., LAWAN R.;
PROC. NATL. ACAD. SCI. U.S.A. 83:2335-2339(1986).
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE, 87091568.
MCLEAN J., WION K., DRAYNA D., FIELDING C., LAWN R.;
NUCLEIC ACIDS RES. 14:9397-9406(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT LEU-34.
MEDLINE; 92134273.
SKRETING G., PRYDZ H.;
BIOCHEM. BIOPHYS. RES. COMMUN. 182:583-587(1992).
          539 POTENTIAL.
77274 MW; F0D06821 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 88050946.
TATA F., CHAVES M.E., MARKHAM A.F., SCRACE G
MCINEYRE N., WILLIAMSON R., HUMPHRIES S.E.;
BIOCHIM. BIOPHYS. ACTA 910:142-148(1987).
                                                                                                                                        440 AA
  POTENTIAL
                                                                                        10 VPLPLLLGGLALLAAGVDADVLLEACC 37
                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 17-440 FROM N.A. MEDLINE; 88050946.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 13-440 FROM N.A. MEDLINE; 88049652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN SCI. 4:791-803(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANTS ILE-147 AND MET-371
                                      Query Match 10.7%;
Best Local Similarity 57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYDRATE-BINDING SITES
                                                            16; Conservative
                                                                                                                                      STANDARD;
                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN)
535 5
539 5
703 AA;
                                                                                                                                                                                                           ACYLTRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 95338133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BURLINGAME A.L.
                                                                                                                                       LCAT_HUMAN
P04180;
           CARBOHYD
SEQUENCE
  CARBOHYD
                                                            Matches
                                                                                                                             RESULT
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DT 2(
DT 0:
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FUNE H., ASSMANN G.;
HUM. MUTAT. 8:79-82[1996].
-1- FUNCTION: CENTRAL ENZYME IN THE EXTRACELLULAR METABOLISM OF PLASMA
-1- EUDOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE
CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS.
-1- CATALLYIC ACTIVITY: PHOSPHATIDYLCHINE & STEROL = STEROL ESTER +
-1- CATALLYICE SROPHOSPHOGPHOLINE (PALMITOYL, OLEOYL, AND LINOLEOYL CAN
BE TRANSFERRED; A NUMBER OF STEROLS, INCLUDING CHOLESTEROL, CAN
MEDLINE; 90316533.
TARAMELLI R., PONTOGLIO M., CANDIANI G., OTTOLENGHI S., DIEPLINGER H.,
CATAPANO A., ALBERS J., VERGANI C., MCLEAN J.;
HUM. GENET. 85:195-199(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GERDES U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT AS ACCEPTOR). ENZYME REGULATION: APOLIPOPROTEIN A-I IS A POTENT ACTIVATOR FOR
                                                                                                                                                                                                                                                       GOTODA T., YAWADA N., MURASE T., SAKUMA M., MURAYAMA N., SHIMANO H.
KOZAKI K., ALBERS J.J., YAZAKI Y., AKANUMA Y.;
LANCET 338:778-781(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT HIS-164.
BEDLINE: 95331753.
STEYRER E., HAUBENWALLINER S., HOERL G., GIESSAUF W., KOSTNER G.M.,
ZECHNER R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 91315467.
MAEDA E., NAKA Y., MATOZAKI T., SAKUMA M., AKANUMA Y., YOSHINO G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 95221171.
WIEBUSCH H., CULLEN P., OWEN J.S., COLLINS D., SHARP P.S., FUNKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 93163362.
FUNKE H., VON ECKARDSTEIN A., PRITCHARD P.H., HORNBY A.E.,
WIEBUSCH H., MOTTI C., HAYDEN M.R., DACHET C., JACOTOT B., GER
FAERGEMAN O., ALBERS J.J., COLLEONI N., CATAPANO A., FROHLICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! - DISEASE: DEFECTS IN LCAT ARE THE CAUSE OF NORUM AND FISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OWEN J.S., WIEBUSCH H., CULLEN P., WATTS G.F., LIMA V.L.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS THR-117; TRP-159; CYS-182; PRO-233 AND MET-345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS ARG-57 AND 10 AA INSERTION IN POSITION 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ή.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOCHEM. BIOPHYS. RES. COMMUN. 178:460-466(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKRETIING G., BLOMHOFF J.P., SOLHEIM J., PRYDZ FEBS LEII. 309:307-310(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
EMBL; M12625; G307117; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 93305754.
HILL J.S., O K., WANG X., PRITCHARD P.H.;
BIOCHIM. BIOPHYS. ACTA 1181:321-323(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X06537; -; NOT_ANNOTATED_CDS
EMBL; M26268; G187025; -
EMBL; X04981; G34287; -.
EMBL; M17959; G386858; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLIN. INVEST. 91:677-683(1993).
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                                                                                                                                                                             VARIANTS LYS-252 AND ILE-317. MEDLINE; 92016763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IUM. GENET. 96:105-109(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS THR-117 AND CYS-182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A00571; XXHUN.
PIR; A29661; A29661
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STRAIN=RD / KW20;
MEDLINE; 95350630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PASTEURELLACEAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; HI0412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LT 11
LCAT_PAPAN
Q08758;
                                                                                                                                                                                                                                                                                  LT 10
YCEC_HAEIN
P44433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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CONTRACTOR OF SECULAR AND SECULAR 
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MERONI G., MALGARETTI N., MAGNACHI P., TARAMELLI R.;
SUBMITTED (MAY-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1- FUNCTION: CENTRAL ENZYBE IN THE EXTRACELLULAR METABOLISM OF PLASMA LIPOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE
                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00120; LIPASE_SER; 1.
TRANSFERASE; ACYLTRANSFERASE; LIPID METABOLISM; GLYCOPROTEIN; SIGNAL.
-!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, PLACENTA, LUNG, SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LECITHIN-CHOLESTEROL ACYLTRANSFERASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT AS ACCEPTOR).
-1- ENZYME REGULATION: APOLIPOPROTEIN A-I IS A POTENT ACTIVATOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
(LECITALIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
(LECITALIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WARDEN C.H., LANGNER C.A., GORDON J.I., TAYLOR B.A., MCLEAN J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUS MUSCULUS (MOUSE).
EUKARYOTA; META2OA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
                                                       BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                       Score 88; DB 1; Length 254;
Pred. No. 1.03e+00;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                 EMBL: U03398; G571323; -.
PROSITE; PSO0251; THF_1; 1.
PROSITE; PSO5049; THF_2; 1.
CYTOKINE; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
9E6B904A CRC32;
                                                                                                                                                                                                                                                                                                                  C68C1B27 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIOL. CHEM. 264:21573-21581(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1990 (REL. 15, CREATED)
                                                                                                                                                                                                                                                                                                                  254 AA; 26624 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49765 MW;
                                                                                                                                                                                                                                                                                                                                                                          9.88.6
                                                                                                                                                                                                                                                                                                                                                                                                 66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VPWAAVT-LLLLLLLPPA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 LPWALVAGLLLLLLLAAA 44
                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 66.7%;
les 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J05154; G293697; -.
EMBL; X54095; G52874; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                             MUSCLE AND KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              408
438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A34158; XXMSN.
MGD; MGI:96755; LCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90094326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THIS ENZYME.
                                                       - ! - SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LCAT_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LUSIS A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
DISULFID
DISULFID
                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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SSSEREES
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HIXSON J.E., DRISCOLL D.M., BIRNBAUM S., BRITTEN M.L.;
GENE 128:295-299(1993).
-1- FUNCTION: CENTRAL ENZIME IN THE EXTRACELLULAR METABOLISM OF PLASMA LIPOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAEMOPHILUS INFLUENZAE.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOGGHERTY B.A., MERRICK J.M.,
MCKENNEY K., SUTTON G., FILDHOH W., FIELDS C.A., GOCAYNE J.D.,
MCKENNEY K., SUTTON G., FILLHOH W., FIELDS C.A., GOCAYNE J.D.,
WEIDMAN J.F., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
WHIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
UTTERBACK T.F., HANNA M.C., NGOYEN D.T., SANDEK D.M., BRANDON R.C.,
EINE L.D., FRITCHMAN J.L., FUHRWANN J.L., GEOGHAGEN N.S.M.,
GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
(LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAPIO ANUBIS (OLIVE BABOON).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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  Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VENTER J.C.;
SCIENCE 268:496-512(1995).
-- SIMILARITY: STRONG, TO E.COLI YCEC.
-- SIMILARITY: BELONG TO THE YABO/YCEC/SFHB FAMILY.
EMBL; U32724; G1573385; --
PROSITE; PS01129; YABO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.90e+00;
12; Mismatches 11
  Score 88; DB 1; L
Pred. No. 1.03e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 AA; 36588 MW; AD948C64 CRC32;
                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROTEIN HI0412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 86; DB 1;
                                                                                                                                                                                                                                                                                          Š
                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          440 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.68;
Query Match 9.8%;
Best Local Similarity 75.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 32.4%;
les 11; Conservative
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                                                                                                             7 PWQRVLLLLGLLLPPA 22
                                                                                                                                                                       2 PWAAVTLLLLLLLPPA 17
                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Search completed: Thu Jul 30 09:27:36 1998 Job time: 11 secs.
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BIOCHEMISTRY 27:8443-8448(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ARTIODACIYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
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KESSLER M.A., SCHULER L.A.;
DNA CELL BIOL. 10:93-101(1991).
-!- SUBCELLULAR LOCATION: SECRETED.
-!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE: 90256825.
YAMARAWA M., TANARA M., KOYAWA M., KAGESATO Y., WATAHIKI M.,
YAMAMOTO M., NAKASHIYA K.;
J. BIOL. CHEM. 265:8915-8920(1990).
                                                                                                                                                                                                       Score 86; DB 1; Length 1663;
Pred. No. 1.90e+00;
5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 85; DB 1; Length 236; Pred. No. 2.57e+00; 8; Mismatches 11; Indels
                                                                                                                                                                                                                                                          0; Indels
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94 V -> F (IN REF. 2 AND 3).
170 V -> M (IN G163281).
26908 MW; 88029761 CRC32:
                                                                                                                             LK -> KL (IN REF. 2).
W; 0428CF63 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLACENTAL LACTOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1989 (REL. 10, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
11-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PLACENTAL LACTOGEN I PRECURSOR (BPLE-I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
PROBABLE.
BY SIMILARITY BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. MEDLINE; 89207456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00266; SOMATOTROPIN_1; 1.
PROSITE; PS00338; SOMATOTROPIN_2; 1.
HORMONE; PLACENTA; GLYCOPROTEIN; SIGNAL.
                                                                          PROBABLE. PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                          722 LK .
: 186460 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, JOSEPS, --
EMBL, M33268, G163629, --
EMBL, M65218, G163279, ALT_SEQ.
EMBL, M65219, G163281, ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63277; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G163277; JOINED G163277; JOINED
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Best Local Similarity 38.2%;
Matches 13; Conservative
                                                                                                                                                                                                       Query Match 9.6%;
Best Local Similarity 66.7%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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8 LELELEPPALLSIG 22
                                                                                                                                                                                                                                                                                                             10 LVLLLLLASSLLALG 24
                                                                                                                               721 72
1663 AA;
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  1518
1537
1010
939
1617
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ID PLC1_BOVIN
AC P09611;
                     DISULFID
THIOLEST
CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
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CONFLICT
SEQUENCE
DISULFID
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C STRAINED:

XM MEDLINE; 9144351.

ARPIGNY J.L., FELLER G., GERDAY C.;

BIOCHIM. BIOPHYS. ACTA 1171:331-333(1993).

C -!- FUNCTION: CATALYZES LIPOLYSIS AT TEMPERATURES AS LOW AS 3 DEGREES

C CELSIONS.

C -!- CATALYTIC ACTIVITY: TRIACYLGLYCEROL + H(2)O = DIACYLGLYCEROL +

C A FATTY ACID ANION.

R MALL: X677.12; G74876; -.

R PIR; S28426; S28486.

PIR; S28425; S28225.

R PIR; S28425; S28486.

PR PIR; S28486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
LIPASE 1.
POTENTIAL.
CHARGE RELAY SYSTEM (BY SIMILARITY).
50684A86 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                     PSYCHROBACTER IMMOBILIS.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
NEISSERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                        LIP1_PSYIM STANDARD; PRT; 317 AA.

002104;
01-01-1933 (REL. 26, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
LIPASE 1 PRECURSOR (EC 3.1.1.3) (TRIACYLGLYCEROL LIPASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 85; DB 1; Length 317; Pred. No. 2.57e+00; 9; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 AA; 35251 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.5%;
Best Local Similarity 35.1%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Thu Jul 30 09:26:50 1998; MasPar time 7.38 Seconds 608.699 Million cell updates/sec

protein - protein database search, using Smith-Waterman algorithm

MPsrch\_pp

llar output not generated. Run on:

>US-08-938-548A-10 (1-123) from USO8938548A.pep 899 1 VPWAAVTLLLLLLLPPALLS......GRGCPTVTTALAPRGGSGV 123 Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

120441 seqs, 36531193 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir56
1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d Database:

Mean 39.443; Variance 86.453; scale 0.456 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		æ					
Result	Score	Query Match	Length	DB	8	Description	Pred. No.
	101	11.2	131	-	SEPG	secretin precursor -	9.71e-02
7	98	10.9	641	~	A45054	probable intercellula	2.32e-01
m	96	10.7	601	7	B36346	fibulin 1 precursor,	4.12e-01
4	96	10.7	683	7	C36346	fibulin 1 precursor,	4.12e-01
5	92	10.2	838	~	145557	eyeless, long form -	1.27e+00
9	91	10.1	440	Н	XXHUN	•–	1.68e+00
7	91	10.1	602	~	S39782	cyclooxygenase 1 - ra	1.68e+00
80	89	6.6	602	~	869198	prostaglandin G/H syn	2.91e+00
O	68	9.9	1061	Н	OYHUAR	natriuretic peptide r	2.91e+00
10	88	9.8	245	~	S43293	FLT3/FLK2 ligand (clo	3.81e+00
11	88	9.8	438	Н	XXMSN	-	3.81e+00
12	88	9.8	491	~	JC6197	stromelysin 3 (EC 3.4	3.81e+00
13	87	9.7	583	~	150518	DNA binding protein E	4.99e+00
14	87	9.7	599	~	A36746	prostaglandin-endoper	4.99e+00
15	86	9.6	322	~	G64151	hypothetical protein	6.52e+00
16	98	9.6	410	~	S74705		6.52e+00
17	98	9.6	440	~	JC1502	phosphatidylcholine	6.52e+00
18	98	9.6	497	~	S43745	phosphatidylinositol-	6.52e+00
19	98	9.6	1663	-	C3RT	complement C3 precurs	6.52e+00
20	85	9.5	236	~	A37930	placental lactogen pr	8.50e+00
21	82	9.5	317	~	S28225	triacylglycerol lipas	8.50e+00
22	82	9.5	317	~	S57275	triacylglycerol lipas	8.50e+00
23	82	9.5	334	7	S16296	υ	8.50e+00

8.50e+001 1.11e+01	1.44e+01 1.44e+01 1.44e+01
collagen alpha chain gene E protein - phage protein 108 precursor complement subcompone triacylglycerol lips hypothetical 36.0K pr lutropin-choriogonado lutropin-choriogonado lutropin-choriogonado grass-activating pro Grass-activating pro Grass-activating pro Grass-activating pro Grass-activating pro Hutropin-choriogonado hypothetical protein talin - mouse maltase-like protein serum albumin precurs hypothetical protein serum albumin precurs	immediate-early prote immediate-early prote peptidyl-dipeptidase
\$28774 \$288874 \$47060 \$264055 \$26409 \$14276 \$14276 \$1344 \$41344 \$41344 \$41344 \$4132 \$4132 \$4132 \$6123 \$11661 \$55362 \$73248	EDBE23 EDBE22 S35484
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1002 901 901 1001 1001 3329 3329 3329 7006 6498 6498 6498	676 676 1309
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### ALIGNMENTS

SEPG #type complete secretin precursor - pig #formal_name domestic pig #formal_name sus scrofa domestica #common_name domestic pig 24-Apr-1994 #sequence_revision 12-Apr-1996 #text_change B35094; A01544; A36052	A35094 ROPIN A.S.; Wheeler, M.B.; Leit Ropin, A.S.; Wheeler, M.B.; Leit Proc. Natl. Acad. Sci. U.S.A. (1 Secretin: structure of the precu of the mRNA. erences MUID:90192795 B35094 ule_type mRNA use 1131 ##label KOP	eren ule_	Exercise Associated and associated as a secreting precursor from porcine intestine.  #coession Associated as a secreting precursor from porcine intestine.  #coession Associated as a secreting precursor from porcine intestine.  #accession Associated as a secreting precursor from porcine intestine.  #accession Associated as a pretainminary #accession as a pretain and a secreting a pretain and a secreting a secreting precursor from porcine and a secreting precursor from porcine and a secreting precursor from precursor from precursor from precursor from a secreting precursor from precurso	
RESULT 1 ENTRY TITLE ORGANISM DATE ACCESSIONS	REFERENCE #authors #journal #title #cross-refere #accession ##molecule	REFERENCE #authors #journal #title #cross refere #accession #accession #accession #amolecule ##molecule	KEFEKENCE #authors #journal #title #cross-refere #accession ###molecule ##molecule ##residues	#authors #authors #journal #title #contents #note CLASSIFICATION KEYWORDS

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##cross-references FlyBase:EBgn0005558
itrons 37/1; 92/2; 371/1; 429/1; 521/1; 639/2
itrons 37/1; 92/2; 371/1; 429/1; 521/1; 639/2
FICATION #superfamily unassigned homeobox proteins; homeobox homology, paired box homology
alternative splicing; DNA binding; homeobox; nucleus; transcribtion regulation
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The isolation and characterisation of a cDNA clone for human lecithin:cholesterol acyl transferase and its use to analyse the genes in patients with LCAT deficiency and fish
#authors Quiring, R.; Walldorf, U.; Kloter, U.; Gehring, W.J.
#journal Science (1994) 265:785-789
#title Homology of the eyeless gene of Drosophila to the Small eye
gene in mice and Aniridia in humans [see comments].
#cross-references MUID:94323757
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phosphatidylcholine--sterol O-acyltransferase (EC 2.3.1.43)
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#title Human lecithin-cholesterol acyltransferase gene: complete gene sequence and sites of expression.
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phospholipid--cholesterol acyltransferase precursor
#formal_name Homo sapiens #common_name man
04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change
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#length 838 #molecular-weight 87662 #checksum 392
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##cross-references GB:M12625; NID:9187022; PID:9307117
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##cross-references GB:X04981; NID:934286; PID:934287
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#cross-references MUID:86205950 #accession A00571
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#cross-references MUID:88049652
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Schindler, P.A.; Settineri, C.A.; Collet, X.; Fielding, C.J.; Burlingame, A.L.
Burlingame, A.L.
Soldering Sci. (1995) 4:791-803
Site-specific detection and structural characterization of the glycosylation of human plasma proteins
lectinhin:cholesterol acyltransferase and apolipoprotein D using HPLC/electrospray mass spectrometry and sequential glycosidase digestion.
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Yang, C.; Manoogian, D.; Pao, Q.; Lee, F.; Knapp, R.D.; Gotto
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J. Biol. Chem. (1987) 262:3086-3091
Lecithin: cholesterol acyltransferase. Functional regions and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic clones
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##residues_type mRNA
##residues_typ 17-256,'H',258-440 ##label TAT
##cross-references GB:X06537; NID:9187024;
##cross-references GB:X06537; NID:9187025
PID:9187025
##note the authors translated the codon CAT for residue 241 as
Ile and CAG for residues 251, 304, 368, 373, and 384
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acyltransferase; cholesterol; glycoprotein; lipid metabolism;
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Blochem. Blophys. Res. Commun. (1991) 181:93-940
Molecular defect in familial lecithin:cholesterol
acyltransferase (LOAP) deficiency: a single nucleotide
insertion in LCAT gene causes a complete deficient type of
                                                                                                              ##cross-references GB:MI7959; NID:g187026; PID:g386858
NCE A90666
thors Tata, F.; Chaves, M.E.; Markham, A.F.; Scrace, G.D.; Waterfield, M.D.; McIntyre, N.; Williamson, R.; Humphries, Waterfield, M.D.; Actional M.D.; McIntyre, N.; Williamson, R.; Humphries, N.; Williamson, R.; Humphries, M.D.; McIntyre, M.D.; McIntyre, N.; Williamson, R.; Humphries, M.D.; McIntyre, M.D.; McIntyre, N.; Williamson, R.; Humphries, M.D.; McIntyre, M.D.; McI
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#product phosphatidylcholine--sterol acyltransferase
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The isolation and characterisation of cDNA and ge
for human lecithin:cholesterol acyltransferase.
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##residues 25-284,'Q',286-333,'Q',335-440 ##label YAN
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##molecule_type mRNA
##residues 13-440 ##label ROG
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ORGANISM
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COMMENT
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                                                                                                                                                                                                                                             Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.;
Zurawski, S.; Bazan, J.F.; Kastelein, R.; Hudak, S.;
Wagner, J.; Mattson, J.; Luh, J.; Duda, G.; Martina, N.;
Peterson, D.; Menon, S.; Shanafelt, A.; Muench, M.; Kelner,
G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik,
A.; Rosnet, O.; Dubreuil, P.; Birnbaum, D.; Lee, F.
Nature (1994) 368:643-648
Growth of haematopoietic stem cells and is encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors Warden, C.H.; Langner, C.A.; Gordon, J.I.; Taylor, B.A.;

#journal J. Blol. Chem. (1989) 264:21573-21581

#title Tissue-specific expression, developmental regulation, and chromosomal mapping of the lecithin:cholesterol acyltransferase gene. Evidence for expression in brain and testes as well as liver.

#cross-references MUID:90094326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-245 ##label HAN the codon AGT for residue 25 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XXMSN #type complete
phosphatidylcholine--sterol O-acyltransferase (EC 2.3.1.43)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, July 1990
Promoter and 5' flanking sequences of the mouse LCAT gene. 521370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues 1-438 ##label WAR ##cross-references GB:J05154; NID:g198759; PID:g293697 ##cross-references GB:J05154; NID:g198759; PID:g293697 ##note the authors translated the codon ATG for residue 411
                                                                                          phospholipid-cholesterol acyltransferase precursor;
#formal_name Mus musculus #common_name house mouse
30-8ep-1993 #sequence_revision 30-8ep-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
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#length 245 #molecular-weight 27404 #checksum 295
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lecithin--cholesterol acyltransferase precursor;
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35
                                   8 LLLLLLLPPALLSL-GVDAQPL 28
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14 LLLLLLLPPLLLLLRGSHAGNL
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##residues 1-24:
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#accession
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##cross-references EMBL:X54095; NID:952873; PID:952874

The active enzyme catalyzes the transfer of acyl groups from lecithin to sterol to form sterol esters. Palmitcyl, oleoyl, and linoleoyl residues can be transferred; a number of sterols, including cholesterol, can act as acceptor. Apolipoprotein A-I is a potent activator for this enzyme.

[FICATION #superfamily phosphatidylcholine--sterol avyltransferase]
                                                                                                                                                                                                              acyltransferase; glycoprotein; lipid metabolism; lipoprotein
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##cross-references GB:U46034

This protein is a member of the matrix metalloproteinase family.
FICATION #superfamily interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase homology homology matrix metalloproteinase homology hydrolase; metalloproteinase; zinc; zymogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #domain matrix metalloproteinase homology #label MMP\
#domain hemopexin repeat homology #label PXN\
#binding_site zinc, catalytic (Cys, His, His, His)
(inhibited) #status predicted\
#binding_site zinc, catalytic (His) (active) #status
                                                                                                                                                                                                                                                                        #domain signal sequence #status predicted #label SIG\
                                                                                                                                                                                                                                                                                                   #product phosphatidylcholine--sterol acyltransferase
#status predicted #label MAT\
#binding_site carbohydrate (Asn) (covalent) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UC6197
Okada, A.; Saez, S.; Misumi, Y.; Basset, P.
Gene (1997) 185:187-193
Rat stromelysin 3: CDNA cloning from healing skin wound,
activation by furin and expression in rat tissues.
Skin wounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stromelysin 3 (EC 3.4.24.-) - rat
#formal_name Rattus norvegicus #common_name Norway rat
11-Apr-1997 #sequence_revision 09-May-1997 #text_change
20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150518 #type complete
DNA binding protein E12 - zebra fish
#formal_name Brachydanio rerio #common_name zebra fish
13.5ep-1996 #sequence_revision 13.5ep-1996 #text_change
16.Feb-1997
150518; $49141
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Pred. No. 3.81e+00;
16; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 88; DB 1; Length 438; Pred. No. 3.81e+00;
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#length 491 #molecular-weight 55511 #
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                                                                                                                                                                                                                                                                                                                                                                                           predicted #length 438 #mol
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Best Local Similarity 75.0%;
Matches 12; Conservative
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Best Local Similarity 35.0%;
Matches 21; Conservative
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:26:03 1998; MasPar time 5.63 Seconds 335.050 Million cell updates/sec Run on:

ular output not generated.

>US-08-938-548A-10 (1-123) from USO8938548A.pep 899 1 VPWAAVTLLLLLLLPPALLS......GRGCPTVTTALAPRGGSGV 123 Title: Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

Minimum Match 0% Listing first 4:5 summaries

124785 seqs, 15338987 residues

Searched:

Post-processing:

Database:

a-geneseq31-2
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part13 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27

Mean 29.422; Variance 127.873; scale 0.230 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

)		d					
Result No.	Score	Query Match	l Query Match Length DB	DB	А	Description	Pred. No.
-	96	10.7	566	- 7	R11148	Fibulin A.	5.13e+00
~	96	10.7	601	~	R11149	Fibulin B.	5.13e+00
m	96	10.7	683	~	R11150	Fibulin C.	5.13e+00
4	91	10.1	440	~	P70134	Natural recombinant h	1.21e+01
'n	91	10.1	440	22	W24789	Human lecithin-choles	1.21e+01
9	88	9.8	254	12	R64190	Human 4-1BB-L polypep	2.01e+01
7	88	9.8	254	25	W26657	Human 4-1BB 11gand.	2.01e+01
œ	87	9.7	111	7	R35515	Tryptophan aporepress	2.38e+01
6	87	9.7	599	4	R21690	Prostaglandin endoper	2.38e+01
20	85	9.5	363	23	W12414	Porcine complement in	3.33e+01
11	84	9.3	35		P94256	Truncated E protein f	3.93e+01
12	84	9.3	234	16	R82605	Eph transmembrane tyr	3.93e+01
13	84	9.3	238	13	R71481	Human hek-L protein.	3.93e+01
14	84	9.3	1239	σ	R45945	Glutamic acid recepto	3.93e + 01
15	83	9.5	179	œ	R50056	ICP34.5 fragment.	4.63e+01
16	83	9.5	235	13	R66175	Human S86/Si09 Flt3 1	4.63e+01
17	83	9.5	235	15	R67541	Human flt-3 ligand.	4.63e+01
18	83	9.5	252	7	R21708	HSV-1 (CVG-2) ICP34.5	4.63e+01
19	83	9.5	258	8	R50049	ICP34.5 fragment.	4.63e+01

### ALIGNMENTS

	standard; Protein; 566 AA.		(first entry)		<pre>frin; adhesion; receptor; fibronectin.</pre>			129	/label= signal sequence	30566	/label= fibulin A	86	/label= N-linked glycosylation	535		339	/label- N-linked glycosylation		/Label= type I motii 36 69	/label - repeat unit 1		/label= repeat unit 2		/label= Glu/Asp-rich region		/label type II motif	• :	/label= repeat unit i	/label- consensus pentapeptide		/label= repeat unit 2		/label= consensus pentapeptide		/label- repeat unit 3		/label= consensus pentapeptide 312354	/label= repeat unit 4	355359
	R11148 stand	R11148;	21-MAY-1991	Fibulin A.	Beta-1 integrin;	Homo sapiens	Key	peptide		protein		modified_site		modified_site	10.000	modified_site	1	region	rection		region		region		region		region	40	TOTANT	region	1	region		region		region	region	,	region
RESULT	ß	Ä	ដ	DE	ΧX	SO	FH	F	F	FJ	E	FI	FI	FT	FT	4	E E	4 I	1	4 6-	i Ei	H	F	Η	E I	4	든 ( 년 (	1	- E	F	FI	FŢ	H	ΕŢ	E	H .	- E	FT	FI

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                                                                                                                                                                                                              residue insertion between cysteines 4 and 5 instead of the usual single residue. Embodied within repeats 5, 6, 7 and 8 is the consensus sequence for Asp and Asn hydroxylation. The 7th repeat contains the consensus O-glycosylation sequence, CXCXPC.

Immediately following ach repeat is a pentapeptide with the consensus sequence XD(IV)(D/N)E. Fibulin binds to the cytopasant change the betal subunit of integrin adhesion creceptors in a cation-dependent, EDTA-reversible manner. It can be used to manipulate adhesion of cells to fibronectin, collagen, with the protein have important diagnostic and therapeutic uses. See also RI1147, RI1148 and RI1150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
the repeat lacking two Cys residues. The same motif is found in albumin, vitamin D-binding protein and alpha-fetoprotein. The disulphide-stabilized loop structure is thought to be conserved. The type II motif, related to repeats found in epidermal growth the nith repeat in the A form is incomplete. Four of the repeats in the nith repeat in the A form is incomplete. Four of the repeats, 2, 4 and 9) differ from the EGF-like motif in having a 4-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 601;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fibulin C.
Beta-1 integrin; adhesion; receptor; fibronectin.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Le
5.13e+00;
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Pred. No. 5.
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/label= signal sequence
30..683
/label= fibulin C
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/label- repeat unit 1
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/label= repeat unit 2
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/label- type II motif
180..214
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261..265
/label= consensus pent
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/label- repeat unit 3
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215..219
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/label= type I motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.7%;
Best Local Similarity 57.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R11150;
21-MAY-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220..260
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Purified fibulin, DNA encoding it and antibodies reactive with it useful as diagnostic and therapeutic component.

Useful as diagnostic and therapeutic component.

Claim 10, Fig 5: 56pp; English.

The fibulin A, B and C forms are identical from their N-terminals to a divergence point at posn. 566 (terminal codon in fibulin A) and stainct, encoding polypeptides of 566, 601 and analysis with on and spacing of the Cys residues revealed two cys repeat lacking two Cys residues. The same motif is found in repeat lacking two Cys residues. The same motif is found in the repeat lacking two Cys residues. The same motif is found in albumin, vitamin D-binding protein and alpha-fetoprotein. The components C3a, C4a and C5s; the inverse is found in albumin, vitamin D-binding protein and alpha-fetoprotein. The disulphide-stabilized loop structure is thought to be conserved. The type II motif related to repeats found in epidermal growth factor precursor is a 6-Cys pattern repeated nine times, although the ninth repeat in the A form is incomplete. Four of the repeats.

(2, 3, 4 and 9) differ from the EGF-like motif in having a 4-6 consensus sequence for Asp and Asn hydroxylation. The 7th repeat consensus sequence for Asp and Asn hydroxylation. The 7th repeat consensus sequence XD(I/V)(D/N)E. Fibulin binds to the cytoplasmic domain of the betal subunit of integrin adhesion receptors in a cation-dependent, EDTA-reversible manner. It can be used to manipulate adhesion of cells to fibronectin, collagen, with the contains the consensus sequence in a cation-dependent, EDTA-reversible manner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laminin, and possibly also other proteins. Antibodies reactive with the protein have important diagnostic and therapeutic uses See also R11147, R11148 and R11149.
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P70134;
P70134;
26-APR-1991 (first entry)
Natural recombinant human lecithin:cholesterol acyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                     consensus pentapeptide
                                                                                                                                                                                                                                                                                                           /label - consensus pentapeptide
               consensus pentapeptide
                                                                                  /label consensus pentapeptide
                                                                                                                                           440..444
/label= consensus pentapeptide
                                                  repeat unit 5
                                                                                                                          /label= repeat unit 6
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/label- repeat unit 8
                                                                                                                                                                                                label - repeat unit 7
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                                                                                                                                                                                                                                                                                                                                                            17-AUG-1990; U04662.
18-AUG-1989; US-395773.
(LJOL-) LA JOLLA CANCER RES.
(AMMA-) AMER NAT RED CROSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruoslahti Ei, Argraves WS;
WPI; 91-087250/12.
N-PSDB; 011010.
                                                                                                                                                                                                                                                                                        ..535
                                                                                                       403..439
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                              360..397
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/label- repeat unit 4

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98 plqeacrrkacs-nlpdplngqvsypngdmlfgsk 131
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                                                                                                                  J04045786-A.
                                                              23-JUL-1992
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                                                  R21690;
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Bourdon M, Lernhardt W, Youderlan P;
WADI: 93-03637704.

Tryptophan aporepressor used in vaccine prodn., etc. - contains
Within its' amino acid sequence, a peptide segment heterologous
to the aporepressor located on aq. solvent-assessible surface
Claim 4 + 20; Page 68 + 72; 82pp; English.

The hybrid protein contg. receptor binding sites is active as ligand
for mammallan cell receptors and can be used for a variety of
applications including treatment of diseases resulting from receptor/
ligand dysfunction, and in vaccine prodn.
                                                          The monoding 4-1BB ligand polypeptide(s) - useful for stimulating T-cell proliferation in vitro, and as research tools
This protein comprises human 4-1BB ligand (4-1BB-L), a novel
C-cytokine capable of binding cell surface receptor 4-1BB (see
C-comprise). Its amino acid sequence was deduced from an isolated
C-comprise and acid sequence was deduced from an isolated
C-comprise and also been identified (see W26656). Human
4-1BB-L polypeptides, especially claimed soluble polypeptides
C-comprising the 4-1BB-L extracellular domain (amino acids 49-254),
can be expressed in transformed host cells. They can be used to
stimulate T-cell proliferation in vitro, as research tools and as
immunostimulants for purifying 4-1BB. They may also be useful as
sequence 254 AA;
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                                                                                                                                                                                                                                                                                                                                                                                           R35515 standard; protein; 111 AA.
R35515;
Typicoplan aporepressor (2.7).
TA; N-terminal; C-terminal; tenascin; ligand; binding site;
                                                                                                                                                                                                                                                                          Length 254;
                                                                                                                                                                                                                                                                          Score 88; DB 25; Length 254
Pred. No. 2.01e+01;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 87; DB 7; Length 111;
Pred. No. 2.38e+01;
18; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61..69
/note= "tenascin ligand binding site"
70.111
/note= "TA C-terminal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..60 /note- "TA N-terminal portion"
                         Smith CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Best Local Similarity 27.6%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                         uery Match
Best Local Similarity 66.7%;
Matches 12; Conservative
                     Alderson MR, Goodwin RG, WPI; 97-502333/46.
N-PSDB; T91025.
                                                                                                                                                                                                                                                                                                                              27 Ipwalvaglillllaaa 44
                                                                                                                                                                                                                                                                                                                                             96 pvelrqwleevllksd 111
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21-JUN-1991; US-720222.
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          IMMA ) IMMONEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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Claim 3; Page 12-14; 20pp; Japanese.
This protein is a porcine complement inhibitor encoded by pMCPCDNA (TRIO99). The DNA is useful for large scale production of the forcembinant porcine complement inhibitor, which is useful for porcine organ transplantation into humans. The DNA clone pMCPcDNA is also useful in the analysis of the promoter region of porcine complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
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WPI; 97-08738,08
WPESDB; 761098
DNA encoding porcine complement inhibitor - useful in porcine organ
                                                                                                                                                                                                                                                                                                                                                The protein sequence of hPES was deduced from the cDNA sequence obth. by screening a human genomic library in EMBL3. hPES can be used to screen anti-inflammatory agents. An anti-body against a peptide specific to hPES can be made, and used for the determination of the protein. Sequence 599 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
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porcine; pig; complement; inhibitor; organ transplantation; analysis; promoter.
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Pred. No. 3.33e+01;
10; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                             prostaglandin endo-peroxide synthase - for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 87; DB 4; Length 599; Pred. No. 2.38e+01; 4; Mismatches 7; Indels
                                                                            Prostaglandin endoperoxide synthase.
Human; hPES; screening; anti-inflammatory; antibody.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 lililippipviladpgaptpvnpcc 36
R21690 standard; Protein; 599 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W12414 standard; Protein; 363 AA.
W12414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NIME-) NIPPON MEAT PACKERS INC. (NIHA-) NIPPON HAM KK.
                                                                                                                                                                                 14-FEB-1992.
13-JUN-1990; 152784.
13-JUN-1990; JP-152784.
(MEIP ) MEIJI MILK PRODS KK.
WPI; 92-101937/13.
N-PSDB; Q23001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 51.9%;
Matches 14; Conservative
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Best Local Similarity 34.3%;
Matches 12; Conservative
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                                                   (first entry)
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19-JUN-1996; JO1704.
20-JUN-1995; JP-178254.
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The Ch

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DNA sequences of HSV-1 strains F (Q50037-38, Q50040-42), 17597+ (G50043-45, Q58777), MGH-10 (Q58778-83), and CVG-2 (Q58784-88) and the predicted open reading frames for ICP34.5 (R50048-58) are compared in Fig 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pisclosure; Page 74-75; 95pp; English.

Programmed cell death may be treated through the use of the HSV-1
gene gammal 34.5 or prod. of its expression, ICP34.5. The gene and
its expression have been demonstrated to be required for HSV-1
neurovirulence, and in partic., to act as an inhibitor of neuronal
programmed cell death which allows for viral replication. Use of
the gene therapy, or the protein itself, can be expected to result
in inhibition of programmed cell death in various neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                       "This line is ommited in the specification"
                                   "This line is ommited in the specification"
                                                                                                          /note= "This line is ommited in the specification"
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WPI; 93-336453/42.
Use of gamma, 34.5 gene or encoded ICP 34.5 - for preventing or
treating programmed cell death in neuronal cells or in screening
                                                                                                                                                                                                                                                     New glutamic acid receptor and gene - for use in analysis of synaptic signal translation, and diagnosis of brain disease claim 1; Page 25-31; 35pp; Japanese.

The sequence shows a glutamic acid receptor. The receptor is useful for the analysis of nerve signal translation; within the synapse, expression of synapse plasticity, nerve cell necrosis, pain structure and brain disease. It can also be used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1239;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 84; DB 9; Length 1239
Pred. No. 3.93e+01;
8; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 83; DB 8; Length 179;
Pred. No. 4.63e+01;
13; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gammal 34.5; ICP34.5; programmed cell death; apoptosis;
neurovirulence; inhibition; viral replication; gene the
neurodegenerative disease; herpes simplex virus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              957 gggrtplarrapqpparpgpaqgrlsptcpehpagtlgm 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 AAGILTLGKRRPGPPGLQGRLQ-RLLQANGNHAAGILTM 89
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R50056 standard; Protein; 179 AA.
                                                                                                                                                                               30-JUN-1992; JP-173155.
(MITU ) MITSUBISHI KASEI CORP.
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Best Local Similarity 32.8%;
Matches 19; Conservative
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Local Similarity 38.5%;
les 15; Conservative
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04-MAY-1994 (first entry)
                                                                       /note= "T
883..891
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31-MAR-1992; US-861233.
(ARCH-) ARCH DEV CORP.
Chou J, Roizman B;
                                     /note=
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

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>US-08-938-548A-10 (1-123) from USO8938548A.pep 899 1 VPWAAVTLLLLLLLPPALLS......GRGCPTVTTTALAPRGGSGV 123 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

63816 seqs, 5850866 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5\_COMB 2:PCT9\_COMB 3:backfiles Database:

Mean 27.378; Variance 125.728; scale 0.218 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

4. 14e+01 4. 85e+01 4. 85e+01 4. 85e+01 4. 85e+01 5. 67e+01 5. 67e+01 5. 67e+01 5. 67e+01 5. 67e+01 6. 64e+01 6. 64e+01 6. 64e+01 6. 64e+01 6. 64e+01 6. 64e+01 6. 64e+01		
Application		1BB Ligand Corporation
Sequence 2, A Sequence 2, A Sequence 2, A Sequence 2, A Sequence 10, Sequence 36, Patent No. 54 Sequence 2, A Sequence 11, Sequence 5, A Seque	; 254 AA.	#6.0.1
PCT - US95 - 1 PCT - US91 - 0 US - 08 - 469 - 1 US - 08 - 469 - 6 PCT - US94 - 0 PCT - US94 - 0 PCT - US94 - 0 US - 08 - 243 - 0 US - 08 - 243 - 0 US - 08 - 243 - 0 US - 08 - 249 - 0 US - 08 - 469 - 0 US - 08 - 465 - 0 US - 08 - 485 - 0 US - 08 - 117 - 0	ALIGNMENTS DARD; PRT	2365929697677177668777177877177777777777777777
2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ES .	Sequence 4, Application 05/08236 Patent No. 567404 GENERAL INFORMATION: APPLICANT: Goodwin, Raymond APPLICANT: Goodwin, Raymond APPLICANT: Smith, Craig A. TITLE OF INVENTION: CYLCKINE NUMBER OF SEQUENCES: 18 CORRESPONDENCE ADDRESS: ADDRESSE: Rathryn A. Ande STREET: 51 University Stre CITY: Seattle STATE: Washington COUNTRY: US ZIP: 98101 ZIP: 98101 COMPUTER: RADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: APPLICATION DATA: APPLICATION NUMBER: US/08/ FILING DATE: 07-May-1994 CLASSIFICATION DATA: APPLICATION NUMBER: US/08/ FILING DATE: 07-May-1993 CLASSIFICATION NUMBER: US/08/ FILING DATE: 07-May-1993 CLASSIFICATION NUMBER: US/08/ FILING DATE: 07-May-1993 CLASSIFICATION NUMBER: 32,17 REFERENCE/DOCKET NUMBER: 2 TELECOMMUNICATION INFORMATION TELEPHONE: (206) 283-0430 TELEPHONE: (206) 283-0430 TELEPHONE: (206) 283-0430 TELEPAX: (206) 283-0430 TELEPAX: (206) 283-0430 TELEPAX: (206) 283-0614 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 254 amino acids
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	-91	nce 4, App Fal No. 5674 Fal Invo. 5674 Fal Invo. 5674 Fal Invo. 5674 Fal Invo. 5674 Fal Invo. 5774 Fal Invo. 57
877777778 87777778 8777778 877778 877778 8	T 1 US-08-236 XXXXXX	Sequence 4, 2 Sequence 4, 2 Sequence 6, 2 Sequence 10, 5 Sequence 6, 2 Sequence 10, 5 Sequence 1
40,000,000,000,000,000,000,000,000,000,	RESULT ID US XX AC XXX XX DT XX	

235 AA

STANDARD;

LT 5 PCT-US94-05365-6

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Sequence 3, Application US/08026138E
Patent No. 5502166
GENERAL INFORMATION:
APPLICANT: Masayoshi MISHINA
TITLE OF INVENTION: NOVEL PROTEINS AND GENES CODING THE SAME
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nishiohata Residence 1-107
                                                                                                                                                                                                                                                                                                        CORKEES COUNDENCE ADDRESS:
CORKEES COUNDENCE ADDRESS:
STREET: 5214, Nishiohata machi
CITY: Nigata-shi
STREET: 5214, Nishiohata-machi
CITY: Nigata-shi
STREET: Nigata-ken
CONDTRY: JAPAN
ZIP: 951
COMPUTER: NEADABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS v.5
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/026,138E
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 39563/1992
FILING DATE: 26-FEB-1992
APPLICATION NUMBER: JP 215017/1992
FILING DATE: 12-AUG-1992
APPLICATION NUMBER: JP 303878/1992
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hamburg, C.Bruce
REGISTRATION NUMBER: 22,389
REFERENCE/ACCET NUMBER: 22,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: mouse
TISSUE TYPE: brain
PUBLICATION INFORMATION:
AUTHORS: MASAYOSHI MISHINA
TITLE: NOVEL PROTEINS AND GENES CODING THE SAME
RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 to 1239
JENCE 1239 AA; 135308 MW; 8004364 CN;
                                                                              1239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 84; DB 1;
Pred. No. 1.58e+01
                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: F-4551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 986-2340
                                                                                                                                                                         Sequence 3, Application US/08026138E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uss: single strand
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 986-2340
TELEFAX: (212) 953-7733
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1239 amino acids
                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
9.3%;
Best Local Similarity 38.5%;
Matches 15; Conservative
4 AAVTILILILIPP-ALLSI 21
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STRANDEDNESS: sir
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Sequence 6, Application PC/TUS9405365
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         E: Stephen L. Malaska, Immunex Corporation 51 University Street
                                                                                                                                                                                                                                                         COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC Compatible
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05365
FILING DATE: May 24, 1994
CLASSIFICATION:
APPLICATION NUMBER: -to be assigned-
FILING DATE: May 11, 1994
CLASSIFICATION NUMBER: 08/209,502
APPLICATION NUMBER: 08/209, 502
FILING DATE: March 7, 1994
CLASSIFICATION NUMBER: 08/103,407
FILING DATE: December 3, 1993
FILING DATE: December 3, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: August 25, 1993
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
ENCE 235 AA; 26415 MW; 293990 CN;
                                                                                Sequence 6, Application PC/TUS9405365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFRENCE/CDCKET NUMBER: 2813
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 235 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                         ADDRESSEE:
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SEQUENCE

Gaps

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8; Mismatches 15; Indels

4;

Gaps

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APPLICANT: Thomason, Arlen R.;Nicholson, Margery
IIILE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
DERIVED GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5175255
APPLICANT: Thomason, Arlen R.;Nicholson, Margery
TITLE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
                                                                                                                                                                                Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
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Polypeptide Fusion Dimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    282 AA.
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Pred. No. 2.56e+01;
9; Mismatches 4
                                                                                                                                                                              Score 81; DB 3; L
Pred. No. 2.56e+01;
9; Mismatches 4
                                                                                                                                                                                                                                                                                                                                             261 AA
                                                                                                                                                                                                                                              44 LORLLQGDSGKEDGAELDLNMTRSHSGGELES 75
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72 LQRLLQAN-GNH-AAGI-LTMGR-RAGAELEP 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08445847A
Patent No. 5705484
GENERAL INFORMATION:
APPLICANT: Thomason, Arlen R.
ITILE OF INVENTION: Biologically AC
ITILE OF INVENTION: Polypeptide Fus
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/25,344
FILING DATE: 23-MAR-1987
                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/25,344
FILING DATE: 23-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 241
SEQUENCE 261 AA; 29370 MW; 369384 CN;
                                                                                                                                 LENGTH: 241
SEQUENCE 261 AA; 29326 MW; 367179 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08445847A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1840 Dehavilland Dr. CITY: Thousand Oaks STATE: California
                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                              Match 9.0%;
Local Similarity 46.9%;
hes 15; Conservative
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Best Local Similarity 46.9%;
Matches 15; Conservative
                                                  NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DERIVED GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5175255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-445-847A-1
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                                                                                                                SEQ ID NO:8
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5175255-2
                                                                                                                                                                                 Query Match
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Matches
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Patent No. 5175255
APPLICANT: Thomason, Arlen R.;Nicholson, Margery
IIILE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MURRAY, MARK J.;KELLY, JAMES D.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE MOSAIC PROTEINS
NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
                                                                                                                                                                                 Score 82; DB 3; Length 220;
Pred. No. 2.18e+01;
....matches 6; Indels
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                                                                                                                                                                                                                                                                                 .56e+01;
                                                                                                                                                                                                                                                             23 LORLLHGDPGEEAGAELDLNMTRSHSGGELESLA-RGR 59
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Pred. No. 2.56e+0
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                                                                                                                                                                                                                                                                                                                                                            245 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/319,776 FILING DATE: 07-OCT-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 LORLLQGDSGKEDGAELDLNMTRSHSGGELES 60
                                                               NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/25,344
FILING DATE: 23-WAR-1987
                                                                                                                                                                238 AA; 26810 MW; 307752 CN;
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SEQUENCE 245 AA; 27563 MW; 324570 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 926,149
FILING DATE: 05-ANG-1992
APPLICATION NUMBER: 379,239
FILING DATE: 11-UTL-1989
APPLICATION NUMBER: 941,970
FILING DATE: 15-DEC-1986
APPLICATION NUMBER: 896,485
FILING DATE: 3-ANG-1986
APPLICATION NUMBER: 705,175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    660,496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.0%;
Best Local Similarity 46.9%;
Matches 15; Conservative
                                                                                                                                                                                               Query Match 9.1%;
Best Local Similarity 44.7%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 25-FEB-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                  DERIVED GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5498600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5175255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 5175255
                                                                                                                                                LENGTH: 220
                                                                                                                               SEQ ID NO:4:
                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
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5175255-8
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5498600-2
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Gaps

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Sequence 2, Application PC/TUS9505512
GENERAL INFORMATION:
APPLICAMT: Tonks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Phosphatase
NUMBER OF SEQUENCES:
GORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 233 South Wacker Drive, Suite 6300
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: PLOPPY disk
COMPUTER: PRAPALAEL FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: PRAPALAEL FORM:
APPLICATION NUMBER: PCT/US95/05512
FITTING DAMP.
PUT NOT DAMP.
                                                                                                                            1337 AA.
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NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERNCE/DOCKET NUMBER: 27866/31954
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 1337 AA; 146192 MW; 9857375 CN;
                                                                                                                              PRT;
                                                                                                                                                                                                                                                         Sequence 2, Application PC/TUS9505512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 1337 amino acids
amino acid
                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                     23 LLLLLLLPSPLMA 35
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PCT-US95-05512-2
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19 WA-LPLLLLLLRLGQILCAGGTPSPIPD 45

Score 80; DB 2; Length 1337; Pred. No. 3.01e+01; 4; Mismatches 10; Indels

Query Match
Best Local Similarity 46.4%;
Matches 13; Conservative

3 WAAVTLLLLLLLPPALLSLGVDAQPLPD 30

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Search completed: Thu Jul 30 09:28:43 1998 Job time: 7 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:25:01 1998; MasPar time 2.04 Seconds 77.476 Million cell updates/sec

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1 PGPPGLQGRLQRLLQANGNHAAGILTM 27 >US-08-938-548A-9 (1-27) from US08938548A.pep 192 Perfect Score: Description: Sequence:

PAM 150 Gap 15 Scoring table:

63816 seqs, 5850866 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5\_COMB 2:PCT9\_COMB 3:backfiles Database:

Mean 20.122; Variance 80.971; scale 0.249 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Pred. No.	1.86e+01	2.26e+01	2.26e+01	5.81e+01	5.81e+01	5.81e+01	5.81e+01	5.81e+01	5.81e+01	5.81e+01	5.81e+01	5.81e+01	5.81e+01	5.81e+01	5.81e+01	5.81e+01	8.42e+01	8.42e + 01	8.42e+01	8.42e+01	8.42e+01	8.42e+01	8.42e+01
Description	Sequence 3, Applicatio	Sequence 4, Applicatio	10,	Sequence 2, Applicatio	Sequence 2, Applicatio	4	Sequence 2, Applicatio	œ	Sequence 4, Applicatio	4	4	14,	Sequence 14, Applicati	Sequence 14, Applicati	7,	4, A	•	Sequence 43, Applicati	10,	Patent No. 5215895.	Patent No. 5215895.	Sequence 2, Applicatio	۲,
·	PCT-US91-0	PCT-US95-1	US-08-469-	PCT-US93-0	US-07-941-	US-07-949-	US-08-115-	US-08-792-	US-08-017-	US-08-115-	PCT-US93-0	US-08-165-	US-07-921-	US-07-745-	PCT-US94-1	US-07-941-	-944-40-sn	us-08-062-	US-07-924-	5215895-4	5215895-3	US-08-017-	US-07-949-
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Length	10	716	2509	199	199	199	199	199	199	296	296	296	296	296	296	296	56	27	27	199	199	199	199
% Query Match	34.4	33.9	33.9	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	30.2	30.2	30.2	30.2	30.2	30.2	30.2
Score	99	65	65	9	9	9	9	9	9	9	9	9	9	9	9	9	28	28	28	28	58	28	28
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Patent No. 5498600.  Patent No. 5175255.  Sequence 1, Applicatio Sequence 3, Applicatio Sequence 2, Applicatio Sequence 3, Applicatio Sequence 1, Applicatio	
5498600-2 5175255-8 Pai- 105-08-445-5 See 08-08-186-5 See 08-08-186-5 See 08-08-186-5 See 08-08-186-5 See 08-08-446-5 See 08-08-486-5 See 08-08-5 See	
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### ALIGNMENTS

Sequence 3, Application PC/TUS9104588
GENERAL INFORMATION:
APPLICANT: Browning, Jeffrey
APPLICANT: Ware, Carl F.
TITLE OF INVENTION: SURFACE COMPLEXED LYMPHOTOXIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O Fish & Neave
STREET: 875 Third Avenue, 29th Floor
CITY: New York
STATE: New York 10 AA. PRT; Sequence 3, Application PC/TUS9104588 STANDARD; PCT-US91-04588-3 XXXXX RESULT ID PC 

CITY:
STATE: New ...
COUNTRY: USA
ZIP: 10022-6250
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TAREADABLE FORM:
CC CURRENT APPLICATION PATA:
CC CURRENT APPLICATION NUMBER: PCT/US91/04588
FILING DATE: 19910627
CC FILING DATE: 19910627
CC PRIOR APPLICATION DATA:
CC RESIFICATION NUMBER: US 07/544,862
FILING DATE: 27-JUN-1990
CC ATONER/AGENT INFORMATION:
CC REGISTRATION NUMBER: 27,794
CC REGISTRATION NUMBER: 27,794
CC REGISTRATION NUMBER: B129CIP
CC REGISTRATION NUMBER: B120CIP
CC REGISTRATION NUMBER: B

TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: AMINO ACID TYPE: AMI TOPOLOGY:

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3; Mismatches
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APPLICATION NUMBER: US/07/949,516A
FILING DATE: 19-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
JENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/07949516A
                                                                                                                                                                                       ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: INTELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 199 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy (
COMPUTER: IBM PC com
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Best Local Similarity 70.0%;
Matches 7; Conservative
CORRESPONDENCE ADDRESS:
                                                                                                                             Pennsylvania
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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COMPUTER REA
                                                                                               CITY: Spr
STATE: Pe
COUNTRY:
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   888888888888888888888888888888888888
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                                                                                                  APPLICANT: Genetics Institute, Inc., APPLICANT: Genetics Institute, Inc., APPLICANT: 87 CambridgePark Drive, APPLICANT: Cambridge, MA 02140, USA TITLE OF INVENTION: Method of Treating Cell Damage or NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESSE: HOWEVER: ADDRESSEE: HOWEVER: STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Patent No. 5460810
GENERAL INFORMATION:
APPLICANT: Williams, David A.
APPLICANT: Clark, Steven C.
TITLE OF INVENTION: Method of Treating Cell Damage or INFERTION: Depletion
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.3%; Score 60; DB 2; Length 199; 70.0%; Pred. No. 5.81e+01; utematches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US93/08247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,372
FILING DATE: 02-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: BAK, MALY E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: INDIApct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
JENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                                                     Sequence 2, Application PC/TUS9308247
GENERAL INFORMATION:
APPLICANT: Genetics Institute, Inc
APPLICANT: 87 CambridgePark Drive,
                                                                                               Sequence 2, Application PC/TUS9308247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/07941372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
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             P.O. Box 457
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Pred. No. 5.81e+01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/07949516A
Patent No. 5700664
GENERAL INFORMATION:
APPLICANT: Yang, Yu-Chung
APPLICANT: Bennett, Frances
TITLE OF INVENTION: A MAMMALIAN CYTOKINE, IL-11
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: DS/07/941,372 FILING DATE: 19920902 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATES: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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: Spring House Corporate Center,
Spring House
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COUNTRY:
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Patent No. 5437863
GENERAL INFORMATION:
APPLICANT: Williams, David A.
APPLICANT: Clark, Steven C.
TITLE OF INVENTION: Method of Treating Cell Damage or TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
                                                         APPLICANT: BENNETT, FRANCES K
APPLICANT: PAUL, STEPHAN R
APPLICANT: PAUL, STEPHAN R
APPLICANT: PAUG, YU-CHUNG
TITLE OF INVENTION: A MAMMALIAN CYTOKINE, IL-11
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFARS - GENETICS INSTITUTE, INC.
STREET: 87 CAMBRIDGEPARK DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 60; DB 1; Length 199;
Pred. No. 5.81e+01;
3; Mismatches 0; Indels
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Spring House Corporate Cntr, P.O. Box 457
                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/017,522A
FILING DATE: 19930212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 AA.
                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MEDINERY, M C
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5174A-DIV
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
SEQUENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                     Sequence 4, Application US/08017522A Patent No. 5371193 GENERAL INFORMATION:
Sequence 4, Application US/08017522A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08115680
                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 199 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 31.3%;
Best Local Similarity 70.0%;
Matches 7; Conservative
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CITY: Spring House
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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CLASSIFICATION:
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COUNTRY: U
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US-08-115-680-4
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Gaps
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GENERAL INFORMATION:
APPLICANT: Genetics Institute, Inc.,
APPLICANT: 87 CambridgePark Drive,
APPLICANT: CambridgePark Drive,
APPLICANT: Cambridge, MA 02140, USA
TITLE OF INVENTION: Method of Treating Cell Damage or
TITLE OF INVENTION: Depletion
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cutr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 296;
                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/115,680
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Pred. No. 5.81e+01;
3; Mismatches 0
                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,372
FILING DATE: 02-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US93/08247
                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: INDIAusa
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-506
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 4:
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CLASSIFICATION:
RICH APPLICATION DATA:
APPLICATION NUMBER: US 07/941,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
PENCE 296 AA, 31769 MW; 414378 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
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ZIP: 19477
COMPUTER READABLE FORM:
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70.0%;
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ID PCT-US93-08247-4
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Search completed: Thu Jul 30 09:25:06 1998 Job time : 5 secs.
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                                                                              Sequence 14, Application US/07745382
Patent No. 5270181
GENERAL INFORMATION:
APPLICANT: MCCOy, John
APPLICANT: LaVallie, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioredoxin and Thioredoxin-Like Molecules
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridge
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                                                                                                                                                                                    Length 296;
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Pred. No. 5.81e+01;
3; Mismatches 0;
                     296 AA.
                                                                                                                                                                                                                                                                                            NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: G15188A
TELECOMMUNICATION INPORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
SEQUENCE 296 AA; 31769 MW; 414378 CN;
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                                                                Sequence 14, Application US/07745382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                     STANDARD;
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Similarity 70.0%;
7; Conservative
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ZIP: 02140
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PCT-US94-14179-14
              US-07-745-382-14
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Matches
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APPLICANT: DELIGATION DELIGATION DELIGATION DELIGATION DELIGANT: DELIGATION DELIGANT: Grant, Kathleen
APPLICANT: Grant, Kathleen
APPLICANT: Grant, Kathleen
TITLE OF INVENTION: PERWALT R.D. PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
TORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: APICALING PARK Drive
CITY: Cambridge
CITY: Cambridge
STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                   CORRENT APPL: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWRARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14179
FILING DATE:
CLASSIFICATION:
ATTORNEY/ACTIVE:
ATTORNEY/ACTIVE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 60; DB 2; Length 296; Pred. No. 5.81e+01; 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Meinert, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEBHONE: (617) 876-1170
TELERAX: (617) 876-581
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
JENCE 296 AA; 31769 MW; 414378 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM IYPE: FLORPY di
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Best Local Similarity 70.0%;
Matches 7; Conservative
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 09:22:53 1998; MasPar time 3.90 Seconds 106.277 Million cell updates/sec

Title: >US-08-938-548A-9
Description: (1-27) from US08938548A.pep
Perfect Score: 192

Periect Score: 192 Sequence: 1 PGPPGLQGRLQRLLQANGNHAAGILIM 27

Scoring table: PAM 150 Gap 15 Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 15:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27

Statistics: Mean 21.806; Variance 86.670; scale 0.252

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Pred. No.	5.96e+01	7.19e + 01	7.19e+01	8.67e+01	8.67e+01	8.67e+01	1.04e+02	1.04e + 02	1.51e+02	1.51e+02	1.51e+02	1.51e+02	1.51e+02						
	Description	"p33" N-terminal (2).	Retinoid X receptor i	Protein (OA-519) cros	KM31-7 precursor.	S. cerevisiae scaur2R	Saccharomyces cerevis	Ecdysone receptor.	DHR23alpha protein.	New polypeptide based	Human alveolar surfac	Sequence deduced from	35kd pulmonary surfac	35kd pulmonary surfac	Sequence of human alv	Genomic sequence of h	Plasmid pASPc-SV(10)	Plasmid pASPcg-SV(10)	Sequence deduced from	Vector PSP 35K-1A-10
SOMERKIES	£	R20235	R99737	W32881	R92050	R67691	W10424	R13793	R32889	R00579	R06331	P80694	P70662	P70663	P60665	P60666	P60441	P60442	P82980	R05091
	DB	4	18	24	16	13	22	ო	ဖ	Н	Н	Н	N	~	m	ო	m	m	Н	N
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	Score	99	65	65	64	64	99	63	63	61	61	61	61	19	61	61	61	19	61	61
)	Result No.	1	7	m	4	ស	9	7	80	σ	10	11	12	13	14	15	16	17	18	19

1.51e+02	1.51e+02	•	1.51e+02	1.51e+02	1.81e+02	1.81e+02	1.81e+02	1.81e+02	•	1.81e+02	1.81e+02	1.81e+02	1.81e+02	1.81e+02	1.81e+02	1.81e+02	1.81e+02	1.81e+02	1.81e + 02	1.81e+02	2.18e+02	2.18e+02	2.18e+02	Α.	2.18e+02	
Human 32K ASP encoded	Human 32K ASP encoded	Human 32K alveolar su	Genomic sequence of h	Human 32K ASP encoded	Human adipogenesis in	Human adipogenesis in	Human interleukin-11	Human interleukin-11	Sequence of a cytokin	Human Interleukin-11	Human adipogenesis in	Human interleukin-11.	E.coli thioredoxin-hu	Thioredoxin from PALT	Thioredoxin/des-Pro-I	Thioredoxin-Interleuk	Fusion protein of IL-	Thioredoxin-IL-11 fus	M. tuberculosis RNA p	Virulence-associated	Thermus aquaticus hea	LexA/NuMA fusion prot	GAL4/HA/NuMA fusion p	Platenolide synthase	Platenolide synthase	
R04215	R04216	R04212	P60661	R04217	R43261	R43262	W02202	R75337	R24436	R50176	R43260	R12314	R45916	R26051	R75762	R50177	R26213	R76812	W05831	R76480	R49835	W21732	W21731	9	W23718	
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248	248	271	271	271	169	177	178	178	199	199	199	199	296	296	296	296	296	296	528	530	510	2192	2272	3724	3724	
31.8	31.8	31.8	31.8	31.8	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	30.7	30.7	30.7	30.7	30.7	
61	61	61	61	61	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	59	29	59	29	53	
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### ALIGNMENTS

Query Match 34.4%; Score 66; DB 4; Length 10; Best Local Similarity 88.9%; Pred. No. 5.96e+01; Matches 8; Conservative 1; Mismatches 0; Indels

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Gaps

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Db 1 glegrigr1 9 ||:||||| Qy 5 GLQGRLQRL 13

RESULT 2

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Query Match 32.8%;
Best Local Similarity 64.3%;
Matches 9; Conservative
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                                                                                                                                                                                  26-FEB-1990; US-485749.
(STRD ) LELAND STANFORD
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08-AUG-1991; US-742127.
(GETH ) GENENTECH INC.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aureobasidin resistance gene, scaur2, promoter - useful for effective prodn. of genes encoding proteins, antisense DNA or RNA, decoy genes or ribozymes in yeast, action sequence is the protein product of the Saccharomyces creevisiae Al31-18C (FERM BP-5529) aureobasidin resistance genes creevistae Al31-18C (FERM BP-5529) aureobasidin resistance genes creevistae Al31-18C (FERM BP-5529) aureobasidin resistance genes creavistae Al31-18C (FERM BP-5529) aureobasidin resistance genes creavistance genes or ribozymes in yeast, e.g. for the industrial scale genes or ribozymes in yeast, e.g. for the industrial scale production of proteins for drug or food use. The promoter's transcription can be regulated by proteins encoded by the production of proteins for drug or food use. The promoter's culture in a complete nutritive medium.
                                                                                   Disclosure; Page 77-84; 110pp; English.
Saccharomyces cerevisiae DKD5D, which is sensitive to aureobasidin, was mutagenized with EMS and genomic libraries of 2 resistant strains were prepared. Resistant gene scauriR (Q75956) from the other. A DNA fragment of scauri was used as a probe to isolate a sensitive gene, scauris (Q75956), from the other. T852A mutation leading to a F158Y conversion gave rise to the resistance 1477 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae aureobasidin resistance protien scaur2.
Aureobasidin; resistance; scaur2; promoter; expression; protein;
DNA; RNA; antisense; decoy; gene; ribozyme; yeast; industrial; PDR;
Pleiotropic; production; transcription; regulation; drug; food.
Saccharomyces cerevisiae AL33-18C.
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New genes regulating aureobasidin sensitivity - used to develop prods. for the diagnosis and treatment of diseases such as
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1477;
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Pred. No. 8.67e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 64; DB 13; Length 147
Pred. No. 8.67e+01;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insect steroid receptor; EcR; hormone; DHR23.
Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
264..329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W10424 standard; Protein; 1477 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TAKI ) TAKARA SHUZO CO LTD.
Kato I, Okado T, Takesako K;
WPI; 97-034382/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 GRLORLLOANGNHAAGILTM 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 GRLQRLLQANGNHAAGILIM 27
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.3%;
Best Local Similarity 40.0%;
Matches 8; Conservative
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Best Local Similarity 40.0%;
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27-MAY-1996; J01415.
30-MAY-1995; JP-154094.
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                                                                mycoses
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Edysteroid dependent regulation of genes in mammalian cells -
for induced expression of heterologous genes
Disclosure; Fig 1; 45pp; English.
This sequence represents an eddysteroid receptor DHR23alpha. DHR23-
alpha is a Drosophila steroid receptor homologue which can function as
alpha is a Drosophila steroid receptor homologue which can function as
alpha is induced upon administration of certain ecdysteroids but not
alpha is induced upon administration of certain ecdysteroids but not
any of the mammalian hormones tested. DHR23alpha has been reported to
regulate transcription of genes containing ecdysone response elements
in Drosophila tissue culture cells treated with 20-0H ecdysone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                          DNA encoding insect steroid receptors - and ligands, for use as benign inducing factors
Claim 24; Page 103; 126pp; English.

The amino acid sequence codes for the (20-OH) ecdysone receptor protein which is part of the insect steroid receptor superfamily. It can be used to screen for ligands specific for the insect steroid receptors which can be used as highly specific and highly active pesticides which are biodegradable. See also Ri3791-Ri3794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ecdysteroid, receptor; DHR23alpha; Drosophila; steroid; receptor;
ligand-dependant; transcription factor; mammalian cell; hormone;
ecdysone response element; ecdysone.
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Pred. No. 1.04e+02;
2; Mismatches 3; Indels
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Pred. No. 1.04e+02;
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/note= "zinc-finger DNA-binding domain 431..651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Putative DNA-binding domain"
                                                                                       /note= "hormone-binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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281..330
                                                                                                                                                                                                                                                                     Hogness DS, Koelle MR, Segraves WA, WPI; 91-281480/38.
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R32889 standard; Protein; 878 AA.
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Similarity 64.3%;
9; Conservative
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                                                                                                                                                                                                                                                    Pulmonary surfactant proteins - used for treating Hyaline Membrane Disease or Respiratory Distress Syndrome.
Claim 1; Page 33-34, 50pp; English.
Gene product may be used in treatment of Hyaline Membrane Disease and Respiratory Distress Syndrome (RDS) in both premature infants and adults eg. cardio-pulmonary operations. The protein products may also be used to raise diagnostic antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pulmonary surfactant proteins - used for treating Hyaline Membrane Disease or Respiratory Distress Syndrome. Claim 1; Page 34A-B; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene product may be used in treatment of Hyaline Membrane Disease and Respiratory Distress Syndrome (RDS) in both premature infants and adults eg. cardio-pulmonary operations. The protein products may also be used to raise diagnostic antibodies.
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35kd pulmonary surfactant protein.
Hyaline membrane disease; respiratiory distress syndrome; RDS.
                                 35kd pulmonary surfactant protein.
Hyaline membrane disease; respiratiory distress syndrome; RDS.
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Pred. No. 1.51e+02;
3; Mismatches 3; Indels
                                                                                                                                                                    (GENE.) Genetics Institute Inc.
(BRIG-) Brigham and Women's Hospital.
Taeusch HW, Cobs KA, Steinbrink DR, Floros J, Phelps DS;
WPI: 87-108682/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENE.) Genetics Institute Inc.
(BRIG-) Brigham and Women's Hospital.
Taeusch HW, Cobs KA, Steinbrink DR, Floros J, Phelps DS;
WPI: 87-108682/15.
N-PSDB; N1010.
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P60665 standard; Protein; 248 AA.
P60665;
P31-JUL-1991 (first entry)
Sequence of human alveolar surfactant protein (hASP)
                                                                                                                                                                                                                                                                                                                                                                                                              Score 61; DB 2; L. Pred. No. 1.51e+02; 3; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P70663 standard; Protein; 248 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 31.8%;
Best Local Similarity 60.0%;
Matches 9; Conservative
               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 gppglpahldeelga 109
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                                                                                                          uy-Ark-1987.
26-SEP-1985; UG-034.
26-SEP-1985; US-781130.
15-AUG-1986; US-897183.
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26-SEP-1986; U02034.
26-SEP-1985; US-781130.
15-AUG-1986; US-897183.
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                   Homo sapiens.
WO8702037-A.
                                                                                                                                                                                                                                         N-PSDB; N71009
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WO8702037-A.
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DAY
DDT 299
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ID P6
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Genomic sequence of human alveolar surfactant protein (hASP)
encoded by genomic DNA, used to obtain pASPcg-SV(10)
Regulatable expression system.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example: Fig 5; 94pp; English.
A regulatable expression system for a coding sequence is the system can process genomic as well as intronless DNA.
Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Fig 6; 94pp; English.

A regulatable expression system for a coding sequence is the system can process genomic as well as intronless DNA. Sequence 248 AA;
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Pred. No. 1.51e+02;
3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                        (BIOT-) BIOTECHN RES PARTNE.
(KUSH/) KUSHNER P J.
KuShner PJ. Cofer CL, Friedman J, Talmadge KD;
N-PSDB; N60571.
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25-NOV-1985; US-801674.
(BIOT-) BIOTECHN RES PARTNE.
(KUSH) KUSHNER P J.
KUSHNER PJ. Cofer CL, Friedman J, Talmadge KD;
N-PSDB; N60572.
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                                                                           Location/Qualifiers
1..20
21..248
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P60666 standard; Protein; 248 AA.
P60666;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Regulatable expression systems
on pMT(E):HS and pASPc-SV(10) Regulatable expression system
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60.0%;
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Best Local Similarity 60.0%;
Matches 9; Conservative
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GPPGLQGRLQRLLQA 16
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25-NOV-1985; US-801674.
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                                                        Homo sapiens.
                                                                                                                                      protein
WO8604920-A.
28-AUG-1986.
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WO8604920-A
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:20:43 1998; MasPar time 3.05 Seconds 271.021 Million cell updates/sec lar output not generated.

>US-08-938-548A-8 (1-33) from US08938548A.pep 256 Title:

1 OPLPDCCROKTCSCRLYELLHGAGNHAAGILTL 33 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

69111 seqs, 25083644 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot35 1:swiss1

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 31.693; Variance 44.992; scale 0.704

#### SUMMARIES

Pred. No.	5.12e-02	1.20e-01	2.76e-01	4.17e-01	6.26e-01	6.26e-01	1.40e+00	1.40e+00	2.07e+00	2.07e+00	2.07e+00	2.07e+00	3.06e+00	3.06e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	6.60e+00	6.60e+00
Description	CASPASE-11 PRECURSOR (	PUTATIVE TRANSMEMBRANE	PUTATIVE ACID PHOSPHAT	60S RIBOSOMAL PROTEIN	SPERM MITOCHONDRIAL CA	PUTATIVE FORKHEAD-RELA	IG ALPHA CHAIN C REGIO	MEIOTIC RECOMBINATION	UDP-GLUCOSE 4-EPIMERAS	UDP-GLUCOSE 4-EPIMERAS	PHOSPHORIBOSYLAMINOIMI	INTERFERON-ACTIVATABLE	HYPOTHETICAL PROTEIN M	MITOCHONDRIAL INHERITA	OMEGA-AGATOXIN IIIA.	OMEGA-AGATOXIN IVB PRE	BOLA PROTEIN HOMOLOG.	AGOUTI SWITCH PROTEIN	AGOUTI SWITCH PROTEIN	AGOUTI SWITCH PROTEIN	VACUOLAR PROCESSING EN	PROTEIN ECSC.	ANGIOTENSINOGEN PRECUR
OI OI	ICEB_MOUSE	NMA_HUMAN	PPAW_CAEEL	R10A_TRYBR	MCS_MOUSE	YUL2_CAEEL	ALC_RABIT	RE11_SCHPO	GALE_RAT	GALE_HUMAN	PURK_PSEAE	IFI5_MOUSE	Y115 METJA	MD12_SCHPO	TX03_AGEAP	TX4B_AGEAP	BOLA_HAEIN	AGSW_VULVU	AGSW_MOUSE	AGSW_HUMAN	VPE_VICSA	ECSC_BACSU	ANGT_MOUSE
DB	-		-4	Н	H	Н	Н		7	H	-	٦	H	7	Н	Н	-1	٦	1	1	<del>, -</del> 1	ч	Н
% Query Match Length DB	373	260	450	214	197	461	299	923	347	348	360	425	155	273	16	83	103	125	131	132	493	236	477
% Query Match	29.3	28.5	27.7	27.3	27.0	27.0	26.2	26.2	25.8	25.8	25.8	25.8	25.4	25.4	25.0	25.0	25.0	25.0	25.0	25.0	25.0	24.6	24.6
Score	75	73	71	70	69	69	67	67	99	99	99	99	65	65	64	64	64	64	64	64	64	63	63
Recult 0.	7	7	٣	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

6.60e+00	9.61e+00	9.61e+00	9.61e+00	9.61e+00	9.61e+00	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01
TETRACYCLINE RESISTANC	UNC-6 PROTEIN PRECURSO	GLUTAMATE (NMDA) RECEP	GLUTAMATE (NMDA) RECEP	SPA2 PROTEIN.	MYOSIN HEAVY CHAIN, NO	GENE 34 PROTEIN.	UREASE OPERON URED PRO	UREASE OPERON URED PRO	HYPOTHETICAL PROTEIN K	TUBULIN BETA CHAIN.	PRPD PROTEIN.	GLYCINE BETAINE TRANSP	DNA REPAIR PROTEIN RAD	HYPOTHETICAL 37.9 KD P	MITOGEN-ACTIVATED PROT	HYPOTHETICAL 51.7 KD P	TETRACYCLINE RESISTANC	HYPOTHETICAL 118.6 KD	DNA POLYMERASE (EC 2.7	HYPOTHETICAL 133.0 KD	THYROGLOBULIN PRECURSO
TET9_ENTFA	UNC6_CAEEL	NME1_RAT	NME1_MOUSE	SPA2_YEAST	MY SO_HUMAN	VG34_HSVEB	URED_KLEAE	URED_KLEPN	Y129_HUMAN	TBB_TRYBR	PRPD_SALTY	BETP_CORGL	RAD5_YEAST	YHO5_YEAST	NTF6_TOBAC	YMT1_CAEEL	TETM_UREUR	YAF3_SCHPO	DPOL_ADE07	YIC6_YEAST	THYG BOVIN
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639	612	1464	1464	1466	1976	160	270	270	406	442	483	595	1169	334	371	471	639	1039	1122	1150	2769
24.6	24.2	24.2	24.2	24.2	24.2	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4
63	62	62	62	62	62	61	61	61	61	61	61	61	61	9	9	9	9	9	9	9	9
24	52	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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	¥		_	(E	PROTEASE)			TETRAPODA;					GAGLIARDINI							3	CRIEKINGE			ASC	(BY SIMILARITY)	(POTENTIAL)	ы							GEN		SUBUNIT		SUBUNIT			 Gu	CRC32
			ATE	PDA'									AGL							800	S			S		S	MIL							ZYMOGEN					IIY	-		
	373		SECUENCE UPDATE)	ANNOTATION UPDATE)	3.4.22) (ICH-3			CHORDATA; VERTEBRATA;												DECLERCO	VAN			J.	ion	OF TWO SUBUNITS	FA								Ä.	CASPASE-11	Ä.	CASPASE-11	SIMILARITY	SIMILARITY	NI) N ^-	7DDB4A63
			E	TIO	~			TEB			1	dS;	Ή.		96)						٠ ۵			IVA	CGT	UBU	ASE							SIS	Ę	ASE	Ä	ASE	IMI	H	z	DB4
	PRT;		DEN	OTA	5.			VER				HYM	ZHO		271:20580-20587(1996)					P.,				ACT	EXE	0	ij						ä	APOPTOSIS;	POTENTIAL	ASP	POTENTIAL	ľΩ		BY S	^	2
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	STANDARD;	r c	35,	35,	ä	CAS					,	BA;		YUAN	.50					AND	NS		69	LVE	R	g	Š		G1575318;	E315510;	CASPL.	CAS	CAS	ROI	7	266	285	373	206	25	-	
	STA				URS	O.R.	ous	ZOA	TIA		ď	×σ	×	Χū	271		Ä		90	>	EMA		61-	M	S S	TER	B	ILY	157	~				д								Š
	į	35;	(REL.	(REL.	PRECURSOR	CASP11 OR ICH3 OR CASPL.	MUS MUSCULUS (MOUSE)	METAZOA;	RODENTIA.		FROM N.A	STRAIN-C57BL/6 X CBA; TISSUE-THYMUS; MEDLINE: 96355393	MIURA M.,	GREENBERG A.H.,	Ξ.		SEQUENCE FROM N.A	ï	MEDLINE; 97190206	VAN DE CRAEN M., VANDENABEELE	VAN LOO G., MOLEMANS		403:61-69(1997).	FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF	RESPONSIBLE FOR APOPTOSIS EXECUTION	SUBUNIT: HETERODIMER	SIMILARITY: BELONGS TO PEPTIDASE FAMILY			Ω 	MGD; MGI:107700;	PS01121;	PS01122;	THIOL	٦	80	267	286	206	254		373
	E) (E)	;cs/800	6	97	ဌ	H	rus			٠	F 120	7BL 963	MIU	Ä	BIOL. CHEM.		FRO	STRAIN-C3H/AN;	971	AEN	:		₹.	õ	NSI	11:	ARI	SE	059463;	X13089;	107	PS0	PS0									m
	MOUSE	P/0343; 008	01-NOV-1997	01-NOV-1997	E-1	g	SCO	EUKARYOTA;	EUTHERIA;		E G	ပို		ERG	نِ		S	ပ္ပ	<u>Ξ</u>	ű	Ö	FIERS W.;	FEBS LETT.	NCT	SPO	BUN	MIL	SPA	<b>U</b> 59	$x_{13}$	GI:	.; ы	<u>.;</u>	HYDROLASE;	_		_		ΙE	Ξ	ij	S E
Н	ቯ	343		Š	PAS	P11	Š	ARY	HER		SEQUENCE	AH	S	ENB	BIO		DEN	AIN	LIN	DE	ន	RS	S	E	Æ			ຽ		ï	≥.	PROSITE;	PROSITE;	ROL	PROPEP	N	PROPEP	Z.	ACT_SITE	ACT_SITE	CONFLICT	SEQUENCE
E4	ICEB_MOU	0 7	1-10	01-	CASPASE-11	CAS	MUS	EUK	EOT	Ξ	SEO	STRAIN-C	WANG	GRE		$\Xi$	SEO	STR	Ä	VAN	VAN	FIE	超	<del>!</del>		-	<del>-</del> -		EMBL;	EMBL;	ă	$^{PRO}$	PR0	HYD	PRO	CHAIN	PRO	CHAIN	ACT	Ä	S	SEC
RESULT			_	_		_				_						_	_			_	_	_	_				٠.	٠.	~	~	~	~	~	~			٠.		<b>.</b> .			~
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29.3%; Score 75; DB 1; Length 373;

Query Match

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Score 67; DB 1; Le
Pred. No. 1.40e+00;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    923 AA; 107418 MW; B51C7725 CRC32;
                                                                                                                                                                                                                                                                                                                                           299 AA; 32256 MW; 594CED7C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
MEIOTIC RECOMBINATION PROTEIN REC11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      923 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 97231330.
LI Y.F., NUMATA M., WAHLS W.P., SMITH G.R.;
MOL. MICROBIOL. 23:869-878(1997).
EMBL; U70737; G1619901; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 CCDIMRCLCLIVNKLSEKSNQTAEILVL 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                       PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 26.2%;
Best Local Similarity 35.7%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       26.2%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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TISSUE-SKELETAL MUSCLE;
MEDLINE; 90384840.
                                                                                                                                                                             CHAIN HAPLOTYPE.
EMBL; X00353; G1576; -.
PIR; A02174; AHRB.
HSSP; P01857; 1PFC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RATTUS NORVEGICUS (RAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22
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2 PLPDCCROKIC-SC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 PFPDCCPANSCCTC
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Best Local Similarity
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RE11_SCHPO
092380:
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GALE_RAT
P18645;
01-M
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAENORHABDITIS ELEGANS.
EUKARYOTA; META20a; ACOELOMATES; NEWATODA; SECERNENTEA; RHABDITIDA.
         OKICTOLAGUS CUNICULUS (RÀBBIT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
ETHERIA; LAGOMORPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 6.26e-01;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                        Length 197;
                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PUTATIVE FORKHEAD-RELATED TRANSCRIPTION FACTOR F26A1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, 027312; G860690; WORMPEP; F26A1.2; CRO2683.
PROSITE; PS00657; PORK_HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK_HEAD_3; 1.
TRANSCRIPTIOL PROTEIN; DNA-BINDING; NUCLEAR PROTEIN; TRANSCRIPTION BEGULATION.
FORK-HEAD.
                                                                                                                                                                                                                                                                                                                                                                Pred. No. 6.26e-01;
                                                                                                                                                                                                                                                                       SELENIUM.
4E56990C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 262 FORK-HEAD.
461 AA; 54171 MW; FB2C37B7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALC_RÁBIT STANDARD; PRT; 299 AA. P01879; 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE) IG ALPHA CHAIN C REGION (FRAGMENT). ORYCTOLAGUS CUNICULUS (RABBIT).
                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL
-!- SIMILARITY: CONTAINS A FORK-HEAD DOMAIN.
STRUCTURE OF THE SPERM MITOCHONDRIA
                                                                                                                                                                                                                                                                                                                                           Score 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                               17 17 S
34 34 S
197 AA; 21015 MW;
                                                                                                                                                                                                                                                                                                                                           27.0%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.0%;
Best Local Similarity 35.3%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 RHVLCKCQLFDVLQVEG 237
                                                                                                                                                                                                                                                                                                                                                                                     10; Conservative
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8 ROKTCSCRLYELLHGAG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                  123 PLKPPCCPQK-CSC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PL-PDCCRQKTCSC 14
                                                                                                                                                                                                                                                                                                                                                           Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 84144059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
ID YUL2_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FULTON L.;
                                                                                                                                                                                                                                                                       BINDING
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셤 à

019802;

Matches

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IMMUNOLOGIC SYSTEM.
-!- THIS IMMUNOSLOBULIN BELONGS TO THE IGA-G SUBCLASS. IT WAS ISOLATED FROM A RABBIT HOMOZYGOUS FOR A2, N80, DE12,15, F71, G75 HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
KNIGHT K.L., MARTENS C.L., STOKLOSA C.M., SCHNEIDERMAN R.D.;
NUCLEIC ACIDS RES. 12:1657-1670(1984).
--- PUNCTION: IG ALPHA IS THE MAJOR IMMUNOGLOBULIN CLASS IN BODY
SECRETIONS. IT MAY SERVE BOTH TO DEFEND AGAINST LOCAL INFECTION
AND TO PREVENT ACCESS OF FOREIGN ANTIGENS TO THE GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZESCHNIGK M., WILCKEN-BERGMANN B., STARZINSKI-POWITZ A.;
NUCLEIC ACIDS RES. 18:5289-5289(1990).
-1- FUNCTION: CATALXZES TWO DISTINCT BUT ANALOGGUS REACTIONS: THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
GALCOGE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 67; DB 1; Length 923;
Pred. No. 1.40e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
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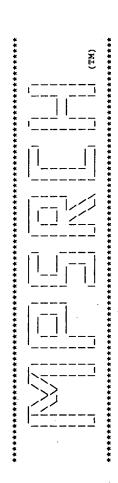
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D., SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAVNE J.D., KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I., OVERBEER R., KIRKNESS B.F., WEINSTOCK K.G., MERRICK J.M., GENDER A., MATTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRNANN J.L., NGUYEN D. R. T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C., M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M., -P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                    METHANOCOCCUS JANNASCHII.
ARCHAEBACTERIA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Pred. No. 3.06e+00;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BERGER K.H., SOGO L.F., YAFFE M.P.;
SUBMITIED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1. SIMILBAILY: TO YEASI MDM12.
EMBL; U64674; G1655884; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 65; DB 1; Lv
Pred. No. 3.06e+00;
2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 AA; 17727 MW; 9D9D61E8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9024B3CC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MD12_SCHPO STANDARD; PRT; 273 AA. Q92377; (REL. 35, CREATED) O1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) O1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) MITOCHONDRIAL INHERITANCE COMPONENT MDM12.
                                                                                                                                          LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REL. 27, CREATED)
(REL. 27, LAST SEQUENCE UPDATE)
(REL. 28, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 A.A.
                                        155 AA
                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                              (REL. 35, CREATED)
(REL. 35, LAST SEQ:
(REL. 35, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 AA; 30517 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CE 273:1058-1073(1996).
U67469; G1498882; -.
                                                                                                                                                                                                                   HYPOTHETICAL PROTEIN MJ0115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 25.4%;
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.4%;
Best Local Similarity 53.3%;
Matches 8; Conservative
                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 CCKITKPCPYRDYEL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 CCR-QKTCSCRLYEL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 LLHGTGEHASSVI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 LLHGAGNHAAGIL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OMEGA-AGATOXIN IIIA
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 96337999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRION.
SEQUENCE 273
                                Y115_METJA
Q57579;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1993
01-FEB-1994
                                                                                                                                          01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P33034;
01-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TX03_AGEAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCIENCE
RESULT
TO YI
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J. BIOL. CHEM. 267:2610-2615(1992).
-1- FUNCTION: OMEGA-AGATOXIN ARE ANTAGONIST OF VOLTAGE-SENSITIVE
CALCIUM CHANNELS. THEY BLOCK INSECT NEUROMUSCULAR TRANSMISSION
CALCIUM CHANNELS. POTENT BLOCKER OF N- AND L-TYPE CALCIUM CHANNELS.
-1- PIM: SIX DISULFIDE BONDS ARE PRESENT (PROBABLE).
PIR: A42335, A42335.
VENOM; NEUROTOXIN, CALCIUM CHANNEL INHIBITOR; PRESYNAPTIC NEUROTOXIN.
SEQUENCE 76 AA; 8518 MW; C7EAOE12 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                          VENEMA V.J., SWIDEREK K.M., LEE T.D., HATHAWAY G.M., ADAMS M.E.;
AGELENOPSIS APERTA (FUNNEL-WEB SPIDER).
EUKARYOTA; METAZOA; ARTHROPODA; CHELICERATA; ARACHNIDA; ARANEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 64; DB 1; Length 76; Pred. No. 4.51e+00; 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 OCCRRNGYCSCYSLFGYLKSG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 DCCROKT-CSC-RLYELLHGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.0%;
similarity 38.1%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conser
                                                                                                                                                          MEDLINE; 92129351.
                                                                                                                             ISSUE-VENOM;
                                                                                          SEQUENCE
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7



MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 09:21:12 1998; MasPar time 5.80 Seconds 239.700 Million cell updates/sec lar output not generated.

1 OPLPDCCROKTCSCRLYELLHGAGNHAAGILTL 33 >US-08-938-548A-8 (1-33) from USO8938548A.pep 256 Description: Perfect Score: Sequence: Title:

PAM 150 Gap 11 Scoring table:

140542 seqs, 42109429 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl5
1:sp\_fungi 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_hur6 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Mean 30.295; Variance 46.908; scale 0.646 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Ouery Match	Query Match Length DB	8	A	Description	Pred. No.
-	77	30.1	363	4	002839	PORCINE MEMBRANE COFAC	5.22e-02
7	74	28.9	750	m	093473	F14B4.1 (FRAGMENT).	1.77e-01
m	73	28.5	683	က	022187	T05A1.3.	2.65e-01
4	73	28.5	1876	m	024453	PHOSPHOINOSITIDE 3-KIN	2.65e-01
S	73	28.5	1876	m	001938	PHOSPHOINOSITIDE 3-KIN	2.65e-01
φ	73	28.5	1876	٣	024209	PHOSPHOINOSITIDE 3-KIN	2.65e-01
7	72	28.1	147	10	061639	3' ORF.	3.94e-01
œ	72	28.1	815	σ	033367	DNA GYRASE B SUBUNIT.	3.94e-01
σ	70	27.3	426	m	001969	SIMILAR TO GALACTOKINA	8.65e-01
10	70	27.3	883	12	091493	DYSTROPHIN (FRAGMENT).	8.65e-01
11	68	26.6	641	σ	048791	TET.	1.87e+00
12	68	26.6	646	σ	048712	TETRACYCLINE RESISTANC	1.87e+00
13	68	26.6	1382	12	090975	TYROSINE KINASE.	1.87e+00
14	99	25.8	479	σ	P94426	HOMOLOGUE OF REGULATOR	3.99e+00
15	65	25.4	197	4	028584	KAP5.5 KERATIN PROTEIN	5.80e+00
16	65	25.4	589	-1	013388	BETA-D-FRUCTOFURANOSID	5.80e+00
17	64	25.0	310	m	001473	COSMID C04E6.	8.38e+00
18	64	25.0	369	σ	P75863	FROM BASES 996879 TO 1	8.38e+00
19	64	25.0	397	6	044258	1-CARBOXY-3-CHLORO-3,4	8.38e+00

8.38e+00

SELD PROTEIN.

3 018373

398

25.0

64

20

8.38e+00 1.21e+01	1.21e+01	1.21e+01 1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	2.47e+01	2.47e+01
SELENOPHOSPHATE SYNTHE REPRESSOR/INDUCER PROT	RIBONUCLEASE.	T21B10.6. F21C3.1.	AMINO ACID TRANSPORTER	TETRACYLINE RESISTANCE	ORF11.	TETM GENE.	LET 858.	SIMILARITY TO EGF-LIKE	NONMUSCLE MYOSIN HEAVY	NONMUSCLE MYOSIN HEAVY	NONMUSCLE MYOSIN HEAVY	DNA FOR DNAJ, COMPLETE	NONMUSCLE MYOSIN HEAVY	NONMUSCLE MYOSIN HEAVY	T24D5.1.	N-METHYL-D-ASPARTATE R	N-METHYL-D-ASPARTATE R	N-METHYL-D-ASPARTATE R	TRKB (FRAGMENT).	MYOSIN HEAVY CHAIN, NO
018597	004393	Q22627 Q19671	039135	067709	057224	047810	017336	018857	027991	012989	027990	033700	062707	062706	022732	012879	063728	008948	091373	002015
ოთო	ာ ထ	m m	ω σ	11	σ	σ	m	ო	7	~	4	σ	10	2	m	7	5	10	12	12
398 146	227	366 405	466	639	639	639	897	2946	66	106	109	157	272	282	304	1464	1464	1464	282	2007
25.0	24.6	24.6 24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	23.8	23.8
4.63	9 9	9 9 9	63	63	63	63	63	63	62	62	62	62	62	62	62	62	62	62	61	61
222	24.	32 7	27	7 6	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

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T 1  O102839  O102839  O102839  O102839  O102839  O102839  O102829  O102839  O102839	ELUINE: 97343414. MEDLINE: 97343414. MEDLINE: 97343414. TOYOMURA K., FUJIMURA T., MURAKAMI H., NATSUME T., SHIGEHISA T., INOUE N., TAKEDA J., KINOSHITA T.; INT. IMMUNOL. 9:869-876(1997). MEMBRANE. MEMBRANE. SEQUENCE 363 Aa; 39692 MW; AD14F57A CRC32;	atch 30.1%; Score 77; DB 4; Length 363; cal Similarity 39.3%; Pred. No. 5.22e-02; ll; Conservative 7; Mismatches 9; Indels 1; Gaps properentary-Misphring 124	DECCRORTES THE TOTAL OF T	01-FEB-1997 (TREMBLREL. 02, CREATED) 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE) 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE) 121404.1 (FRAGMENT). CAENORHABDITIS ELEGANS.	11) SEQUENCE FROM N.A. STEMS M.; SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS. [2] SEQUENCE FROM N.A.
7. 1 002839 002839; 01-JUL- 01-JUL- 01-JAN- PORCINE SUS SCR EUKARYO	SEQU MEDL TOYO TOYO INOU INT. EMBL MEMB	Query Match Best Local Matches	თ	0934 01-F 01-F 01-J CAEN EUKA	(1) SEQU SIMS SUBM [2] SEQU
RESULT  DAC  ODT  ODT  ODE  OCC  E  OCC  E  OCC  OCC  OCC  OC	STREET	Que Bes Mat	SUI		RR RR Rb

**5888** 

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MELSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., WELLINE; 94150718.

WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., COULSON A., BONTIELD J., BURTON J., CONBELL M., COOPER J., COULSON A., GREEN D., LOWELL R., FAVELLO A., FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSTEM J., LISTER N., LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFREN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R. SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., THERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
CHONDRICHTHYES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 70; DB 3; Length 426;
Pred. No. 8.65e-01;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHRITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, AF003739; G2105488; -.
PROSITE; PS00627; GHMP_KINASES_ATP; 1.
SEQUENCE 426 AA; 47290 MW; 7CBEF743 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATTUNG S., GOELA D., WILSON R.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                     CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAVIN A.J., DYER S.M., YEADON J.E., BURDEN S.J.;
J. PHYSIOL, (PARIS) 0:131-133(1991).
EMED: M37645; G397971; -
PROSITE; PS01159; WW_DOMAIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 92064638.
YEADON J.E., LIN H., DYER S.M., BURDEN S.J.;
J. CELL BIOL. 115:1069-1076(1991).
                                                                                                          426 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      883 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQ!
01-JAN-1998 (TREMBLREL. 05, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 ECSCRELDEICRLY-LDHGALGARLTG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | | |: | | | | | | | | : : | 5 DC-CRQKTCSCRLYELLHGA-GNHAAG 29
                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                     01-JUL-1997 (TREMBLREL. 04,
01-JUL-1997 (TREMBLREL. 04,
01-JAN-1998 (TREMBLREL. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 27.3%;
Best Local Similarity 48.1%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                            SIMILAR TO GALACTOKINASE.
                                                                                                                                                                                                                                                                                                                                             CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DYSTROPHIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                    LT 9
001969
001969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 10
091493
091493;
                                                                                                                                                                                                                                                                                                           M01D7.4
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                                                                           RESULT
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SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POIRIER F., CHAN C.T.J., TIMMONS P., ROBERTSON E.J., EVANS M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                             ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
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                                                                                                                                                                 Query Match 28.5%; Score 73; DB 3; Length 1876; Best Local Similarity 41.7%; Pred. No. 2.65e-01; Matches 10; Conservative 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 28.1%; Score 72; DB 10; Length 147; Best Local Similarity 32.1%; Pred. No. 3.94e-01; Matches 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 72; DB 9; Length 815;
Pred. No. 3.94e-01;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYXOCOCCUS XANTHUS.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; MYXOBACTERALES;
MYXOCOCCACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 061639
061639;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
OF DOUBLE-STRANDED DNA.
EMBL; AJ000543; E1168188; -.
PROSITE; PS00117; TOPOISOMERASE_II; 1.
SEQUERASE; TOPOISOMERASE, ATP-BINDING.
SEQUENCE 815 AA; 89636 MW; 65A25520 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 AA; 16309 MW; 6DC857F5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   815 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 CCNONHYTTCLRNLLQGEAERTDGVNIL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CCRQKTCSCRLYELLHGAGNHAAGILTL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                       501 RRKTCT-RLYELISDQRTDDPELL 523
                                                                                                                                                                                                                                                                                                                                                                         8 ROKTCSCRLYELLHGAGNHAAGIL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIGBY P.W.J.;
DEVELOPMENT 113:1105-1114(1991).
EMBL; X58196; G51133; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          691 PSCRRRSTWSCRLCAEHLRGAG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 PDCCRQKTCSCRLY-ELLHGAG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 28.1%;
Best Local Similarity 59.1%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     033367;
03387;
01-JAN-1998 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA GYRASE B SUBUNIT
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SEQUENCE FROM N.A.
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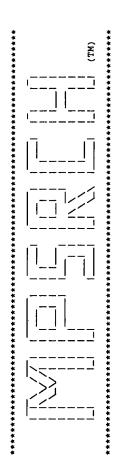
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                                                                                    0; Gaps
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                                                                                                                                                                                                                               OVIS ARIES (SHEEP).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ARTIODACTYLA.
                                                              Score 66; DB 9; Length 479;
Pred. No. 3.99e+00;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                Score 65; DB 4; Length 197;
Pred. No. 5.80e+00;
2; Mismatches 3; Indels
      1
197 AA; 17474 MW; 731C19CA CRC32;
                                                                                                                                                                                                                                                                  INSUENCE FROM N.A.
TISSUE-WOOL FOLLICLE;
MEDLINE; 94358466.
JENKINS B.J., POWELL B.C.;
J. INVEST. DERMATOL. 103:310-317(1994).
EMBL; X73435; G313722; -.
                                                               Query Match
Best Local Similarity 41.2%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                     207 RMYQLLKNAGKQVKTIM 223
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15 RLYELLHGAGNHAAGIL 31
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SEQUENCE
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Search completed: Thu Jul 30 09:21:29 1998 time: 17 secs.

87 VPVCCRVPACSC 98 :| | | | :| | | 3 LPDCCRQKTCSC 14

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 09:20:12 1998; MasPar time 4.75 Seconds 253.613 Million cell updates/sec lar output not generated.

>US-08-938-548A-8 (1-33) from US08938548A.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

Searched:

120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d Database:

Mean 30.310; Variance 51.743; scale 0.586 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Dog 11 1		æ 6					
انوا	Score	Match	Length DB	BB	a	Description	Pred. No.
1	72	28.1	147	N	S24303	hypothetical protein	9.01e-01
~	70	27.3	870	7	A41130	dystrophin homolog -	1.84e+00
m	69	27.0	93	~	860079	oct2 protein isoform	2.63e+00
4	69	27.0	143	7	A37199	sperm mitochondrial c	2.63e+00
ഗ	68	26.6	641	~	JN0800	tetracycline-minocycl	3.73e+00
9	67	26.2	299	Н	AHRB	Iq alpha chain C reqi	5.28e+00
7	67	26.2	338	~	S09276	alpha chain C	5.28e+00
œ	99	25.8	347	~	S11223	Δ.	7.44e+00
0	99	25.8	425	~	156329	gene D3 protein - mou	7.44e+00
ដ	99	25.8	479	7	B69764	transcriptional requi	7.44e+00
Ξ	65	25.4	155	~	C64314	hypothetical protein	1.05e+01
12	65	25.4	197	7	146413	keratin KAP5.5 - shee	1.05e+01
13	65	25.4	589	7	833920	beta-fructofuranosida	1.05e+01
14	64	25.0	35	S	10MB	Omega-aga-ivb (nmr, m	1.46e+01
12	64	25.0	48	'n	10MA	Omega-aga-1vb (nmr, 2	1.46e + 01
16	64	25.0	48	S	1AGG	omega-agatoxin-ivb -	1.46e+01
11	64	25.0	48		A44664	omega-agatoxin IVB -	1.46e+01
18	64	25.0	16	7	B54252	omega-agatoxin III, 8	1.46e+01
13	64	25.0	16	7	A42335	omega-agatoxin IIIA -	1.46e+01
20	64	25.0	76	~	A54252		1.46e+01
7	64	25.0	103	~	B64052	cell division protein	1.46e+01
22	64	25.0	131	~	A46298	pigment deposition co	1.46e+01
23	64	25.0	132	7	137143	agouti protein precur	1.46e+01

1.46e+01	1.46e+01	2.04e+01	2.04e+01	2.04e+01	2.04e+01	2.04e+01	2.04e+01	2.04e+01	2.84e+01	2.84e+01	2.84e + 01	2.84e + 01	2.84e+01	2.84e+01	2.84e+01	3.93e+01	3.93e+01	3.93e+01	3.93e+01	3.93e+01	3.93e+01
hypothetical protein	cysteine proteinase (	hypothetical protein	Idalpha chain C redi	amino acid transport	angiotensin precursor	tetracycline resistan	tetracycline resistan	tetracycline resistan	hypothetical 17.9K pr	u	myosin heavy chain, n	N-methyl-D-aspartate	glutamate receptor, N	N-methyl D-aspartate	SPA2 protein - yeast	omega-agatoxin III, 8	gene 34 protein - equ	urease-associated pro	ureD protein - Klebsi	DNA repair protein RA	myosin heavy chain-B,
B64835	S49175	н69619	S09271	B57479	A29978	S13142	A60633	A56779	JC5551	JH0799	B61231	S47555	S29159	A43274	A36426	D54252	WZBEC7	A42887	S32937	S64859	B43402
~	~	~	~	~	~	7	~	~	~	N	~	~	~	~	~	~	-	~	N	~	Н
369	493	236	360	396	477	639	639	639	157	612	722	1464	1464	1464	1466	16	160	270	270	1169	2007
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25.	25.	24.	24.	24.	24.	24.	24.	24.	24.	24.	24.	24.	24.	24.	24.	23.	23.	23.	23.	23.	23.
64	64	63	63	63	63	63	63	63	62	62	62	62	62	62	62	61	61	61	61	61	61
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

ENENULT ENTRY  BYDOThetical protein H19-3' - mouse ORGANISM  #formal_name Mus musculus #common_name hous DATE 10-5ep-1997 10-5ep-1997 10-5ep-1997 10-5ep-1997 10-6ep-1997 10-6ep-1998 10-6ep-1997 10-6

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CLASSIFICATION
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5-343
SUMMARY
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                                                  *superfamily immunoglobulin C region; immunoglobulin homology duplication; glycoprotein; heterotetramer; immunoglobulin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. (1990) 18:5289 CDNA from rat cells with reconstitutive galactose-epimerase activity in E. coli.
stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zeschnigk, M.; von Wilcken-Bergmann, B.; Starzinski-Powitz
                                                                                                                     #domain immunoglobulin homology #label IGG1\
#domain immunoglobulin homology #label IGG2\
#binding_site carbohydrate (Asn) (covalent) #status
predicted
#length 299 #checksum 2361
                                                                                                                                                                                                                                                                                                                                                                                                                       Ig alpha chain C region - rabbit (fragment)
#formal_name Oryctolagus cuniculus #common_name domestic
                                                                                                                                                                                                                                                               Gaps
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16-Aug-1996
S09276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UDPglucose 4-epimerase (EC 5.1.3.2) - rat
UDPgalactose 4-epimerase
#formal_name Rattus norvegicus #common_name Norway rat
18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.
#journal EMBO J. (1989) 8:4041-4047
#title The 19A heavy-chain gene family in rabbit: cloning and sequence analysis of 13 C-alpha genes.
#cross-references MUID:90076124
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Pred. No. 5.28e+00;
4; Mismatches 2; Indels
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#accession S11223
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ilarity 50.0%; P
Conservative
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Best Local Similarity 50.0%;
Matches 7; Conservative
                                    oligomers.
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2 PLPDCCRQKTC-SC 14
                                                                                                                                                                                                                                                                                                  44 PFPDCCPANSCCTC 57
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                                                                                    plasma
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86-152
189-261
38,286
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Aloni, G.; Azevedo, V.; Bortero, M.G.; Bessieres, P.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolothin, A.; Borchert, S.; Bortss, R.; Boursier, L.; Brans,
A.; Braun, M.; Brignell, S.(C.; Bron, S.; Brouillet, S.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.Devine, K.M.; Duesterhoeft, A.;
Ehlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Erington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;
Guiseppl, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors Tannenbaum, C.S.; Major, J.; Obmori, Y.; Hamilton, T.A.
#journal J. Leukoc. Biol. (1993) 53:563-568
#title A lipopolysaccharide-inducible macrophage gene (D3) is a new member of an interferon-inducible gene cluster and is selectively expressed in mononuclear phagocytes.
#cross_references MUID:93274206
#accession 156329
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#formal_name Mus sp. #common_name mouse
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
28-Feb-1997
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#formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
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UDPglucose 4-epimerase homology
                                                                                                                                                                                                                                           #domain UDPglucose 4-epimerase homology #label [#length 347 #molecular-weight 38225 #checksum 6947
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                                                                                                                                                                                                                                                                                                                                  Length 347;
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Pred. No. 7.44e+00;
4; Mismatches 2; Indels
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##residues
##cross-references GB:S62227; NID:9385702; PID:9385703
##residues 1-347 ##label ZES
##cross-references EMBL:X53949; NID:g57791; PID:g57792
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Local Similarity 53.8%;
Local Similarity 53.8%;
Local 7; Conservative
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Fauthors Yu, H.; Rosen, M.K.; Schreiber, S.L.
#submission submitted to the Brookhaven Protein Data Bank, September 1993
#cross-references PDB:10MB
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#submission submitted to the Brookhaven Protein Data Bank, September 1993
#cross-references PDB:10MA
#domain signal sequence #status experimental #label SIG\
#product beta-fructofuranosidase #status experimental
#label MAT\
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                                                                              #binding_site carbohydrate (Asn) (covalent) #status
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                                                                                           #molecular-weight 3804 #checksum 7419
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                                                                                                                                                                                                      Query Match 25.4%; Score 65; DB 2; Lv
Best Local Similarity 42.1%; Pred. No. 1.05e+01;
Matches 8; Conservative 6; Mismatches 4
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Pred. No. 1.46e-
2; Mismatches
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#region turn (type II)\
#disulfide_bonds\
#disulfide_bonds\
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Best Local Similarity 45.5%;
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Best Local Similarity 45.5%;
Matches 5; Conservative
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254,259,318,322,
388,463,518,527
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#submission
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Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 19 CCRGRPCRCSM 29

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Qy 6 CCRQKTCSCRL 16

Search completed: Thu Jul 30 09:20:24 1998
Job time: 12 secs.
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:21:47 1998; MasPar time 1.31 Seconds 147.949 Million cell updates/sec ular output not generated. :uo cm

>US-08-938-548A-8 (1-33) from US08938548A.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 Title: Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

63816 seqs, 5850866 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

a-issued 1:5\_COMB 2:PCT9\_COMB 3:backfiles

Mean 21.451; Variance 82.349; scale 0.260

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	ВВ	Ð	Description		Pred. No.	
-	99	25.8	39	: ⊣	US-08-249-	Seguence 40, Appl	Applicati	2.23e+01	
~	99	25.8	39	Н	US-08-036-	40,	Applicati	2.23e+01	
m	99	25.8	39	~	PCT-US95-0	40,	Applicati	2.23e+01	
4	99	25.8	39	7	PCT-US94-0	40,	Applicati	2.23e+01	
2	99	25.8	39	Н	US-08-469-	40,	Applicati	2.23e+01	
ø	99 .	25.8	348	~	PCT-US95-0	2, A	catio	2.23e+01	
7	99	25.0	1167	-	US-08-485-	ý	catio	3.29e+01	
œ	64	25.0	1168	Н	US-08-620-	6	catio	3.29e+01	
σ	62	24.2	1464	н	US-08-026-	ì	catio	4.83e+01	
10	61	23.8	42	Н	US-08-487-	23,	icati	5.85e+01	
디	61	23.8	42	Н	US-08-480-	23,	Applicati	5.85e+01	
12	61		42		US-08-477-	23,	Applicati	5.85e+01	
13	61	23.8	42	Н	US-08-137-	23,	Applicati	5.85e+01	
14	61	23.8	59	Н	US-08-233-	51,	icati	5.85e+01	
12	9	23.4	222	m	5223425-6	0.5	5.	7.08e+01	
19	9	23.4	334	Н	US-08-279-	Sequence 10, Appl	Applicati	7.08e+01	
11	29	23.0	283	-	us-08-658-	2,2	catio	8.55e+01	
18	59	23.0	1019	-	US-08-296-	4	catio	8.55e+01	
13	59	3	1083	Н	US-08-296-	7	catio	8.55e+01	
20	57	22.3	21	Н	US-08-019-	'n	catio	1.24e+02	
21	57	22.3	48	-	US-08-379-	٦,	catio	1.24e+02	
22	57	22.3	724	ч	US-08-121-	62,	Applicati	1.24e+02	
23	57	22.3	724	~	PCT-US94-1	62,	Applicati	1.24e+02	

11.24444 12.244444 12.24444444 12.24444444 12.2444444 12.2444444 12.24444 12.244444 12.2444 12.2444 12	ni, Mark;	
Sequence 2, Application Sequence 20, Application Sequence 20, Application Sequence 3, Application Sequence 3, Application Sequence 49, Application Sequence 40, Application Patent No. 5177308.  Patent No. 5475086.  Sequence 1, Application Sequence 12, Application Sequence 12, Application Sequence 12, Application Sequence 14, Application Sequence 17, Application Sequence 2, Application Sequence 3, Application Sequence 2, Application Sequence 3, Application Sequence 2, Application Sequence 3, Application Sequence 3, Application Sequence 3, Application Sequence 4, Application Sequence 5, Application Sequence 6, Application Sequence 6, Application Sequence 7, Ap	PRT; 39 AA.  132A.  Stroobant, Paul; Waterfield, Michael; Marchioni, es, Ian cogenic Factors, Their on and Use inch, 360 kb storage 149,322A.	
1 US-08-363- 1 US-08-446- 1 US-08-446- 1 US-08-357- 2 DCT-US95-1 1 US-08-123- 3 5177308-123- 3 5177308-123- 3 5475086-7- 1 US-08-161- 1 US-08-161-	ALIGNME NDARD; NS/082493 US/082493 US/08249 US/08249 US/08249 US/082493 US/08/28 E. Lunch Avenue Y  M: 5.25 PC-DOS PC-DOS PC-TOS	ON DATA:  UMBER: 07/965,173  33 - OCT - 1992  UMBER: 07/940,389  03 - SEP - 1992  03 - SEP - 1992  UMBER: 07/907,138  30 - JUN - 1992  ON DATA:
22.33 22.33 22.33 22.33 22.33 22.33 23.33	CXXX  CXXX  Tuence 40, Application US/08  quence 40, Application US/08  APPLICANT: Minghetti, Lu ADRESSEE: Rele 4 Lyn STREET: 1080 Third Aven CITY: New York City STREET: 1002  STREET: 1002  COUNTRY: USA ZIP: 1002  CONFUTER READABLE FORM: MEDIUM TYPE: DISKETC, COMPUTER READABLE FORM: MEDIUM TYPE: 20-MAY-19  CLASSIFICATION NUMBER: US, FILING DATE: 26-MAY-19  CLASSIFICATION DATA: PRICATION DAT	PRIOR APPLICATION DATA: APPLICATION NUMBER: 07, FILING DATE: 23-0CT-199 FILING DATE: 30-0CT-199 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07, PRIOR APPLICATION DATA: APPLICATION NUMBER: 07, FILING DATE: 30-JUN-199 FRIOR APPLICATION DATA:
5.5.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2		PRIOR APPLICE APPLICE FILING PRIOR APPLICE FILING PRIOR APPLICE APPLICE APPLICE APPLICE FILING FILING
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Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
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                                                                                                                                                    TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                         8 CCR-TICACR 16
                                                                                                                                                                                                                                                                                                          6 CCRQKTCSCR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                 US-08-469-569-40
                                                                                                                                                                                                SEQUENCE
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ID US
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                                                                                                                                                                                                                                                                                                                                                                                 Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 40, Application PC/TUS9405083C
GENERAL INFORMATION:
APPLICANT: Robert Sklar, Mark Marchionni,
APPLICANT: David I. Gwynne
TITLE OF INVENTION: METHODS FOR ALTERING
TITLE OF INVENTION: MUSCLE CONDITION
NUMBER OF SEQUENCES: 185
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                 Score 66; DB 2; L. Pred. No. 2.23e+01; 1; Mismatches 1
                                                                                                                                                                 NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5250.5
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 39
                                        FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
PRIOR APPLICATION NUMBER: U.K. 91 07566.3
FILING DATE: 10-APRIL-1991
ATTORNEY_AGENT INFORMATION:
NAME: Hanson, Norman D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360
MEDIUM TYPE: kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SIGNEM: PC-DOS
SOFTWARE: WOrdberfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US94/05083C
FILING DATE: 06-MAY-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 40, Application PC/TUS9405083C
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,204
FILING DATE: 08-MAR-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059,022
FILING DATE: 06-May-93
         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
CE 39 AA; 3760 MW; 6521 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
FILING DATE: 03-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
STATE: Massachusetts
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                               25.8%;
Similarity 70.0%;
7; Conservative
                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity
Matches 7; Conser
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ID US-08-026-138E-1
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Sequence 1, Applic
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TABLE OF INFORMAT
C
TITLE OF INVENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                             Query Match
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Patent No. 5670365
GENERAL INFORMATION:
APPLICANT: Feitelson, Jerald S.
TITLE OF INVENTION: Identification of, and Uses For, Nematicidal
TITLE OF INVENTION: Bacillus thuringiensis Genes, Toxins, and Isolates
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
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                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                        Score 64; DB 1; Length 1167;
Pred. No. 3.29e+01;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                        1168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/540,104
FILING DATE: 06-0CT-1995
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: SALIWANGCHIK, DAVIG R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA48DD2.C1 TELECOMMUNICATION INFORMATION:
                                                                                                                                              MOLECULE TYPE: protein
FENCE 1167 AA; 131657 MW; 7095219 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,717A
                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: MA94.C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08620717A
                         TELEPHONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 6: SEGUENCE CHARACTERISTICS:
LENGTH: 1167 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (352) 375-8100
TELEPAX: (352) 372-5800
INFORMATION FOR SEG ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1168 amino acids
                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                       Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                  873 PNCCKPAACQC 883
                                                                                                                                                                                                                                                                                                                         us-08-620-717A-9
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4 PDCCRQKTCSC 14
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                                                                                                                                                               SEQUENCE
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 88888888888888
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Gaps
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Patent No. 5502166
Patent No. 5502160:
APPLICANT: Masayoshi MISHINA
APPLICANT: Masayoshi NOVEL PROTEINS AND GENES CODING THE SAME NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                             ö
                                                                        Length 1168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSE: Nishiohata Residence 1-107
STREET: 5214, Nishiohata-machi
CITY: Nijgata-shi
STATE: Nijgata-ken
COUNTRY: JAPAN
ZIP: 951
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM Compatible
COMPUTER: MS-DOS V.5
                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE: NOVEL PROTEINS AND GENES CODING THE SAME RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 to 1464 KCE 1464 AA; 165489 MW; 11224000 CN;
                                                                                                                                                                                                                                                                                                                          1464 AA
                                                                        Score 64; DB 1; L
Pred. No. 3.29e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/026,138E
FILING DATE: 26-FEB-1993
APPLICATION NUMBER: US/08/026,138E
FILING DATE: 26-FEB-1992
APPLICATION NUMBER: UP 39563/1992
FILING DATE: 36-FEB-1992
APPLICATION NUMBER: UP 215017/1992
FILING DATE: 12-AUG-1992
APPLICATION NUMBER: UP 215017/1992
FILING DATE: 12-AUG-1992
APPLICATION NUMBER: UP 303878/1992
FILING DATE: 13-NOV-1992
ATTONNEY, AGENT INFORMATION:
NAME: Hamburg, C. Bruce
REGISTRATION NUMBER: 22,389
                                                                                                                           3; Mismatches
INDIVIDUAL ISOLATE: 167p
SEQUENCE 1168 AA; 131542 MW; 7175894 CN;
                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08026138E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: F-45
TELECOMMUNICATION INFORMATION:
TELEFHONE: (212) 986-2340
TELEFAX: (212) 986-3340
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single strand TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: mouse
TISSUE TYPE: cerebellum
PUBLICATION INFORMATION:
AUTHORS: Masayoshi MISHINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1464 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                      Query Match 25.0%;
Best Local Similarity 45.5%;
Matches 5; Conservative
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XXXXXX

RESULT

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APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Santos, Ameurfina D.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: TOWNERS AND TYPE TOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 61; DB 1; Length 42;
Pred. No. 5.85e+01;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,800
FILING DATE: 19-COT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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APPLICANT: DOTAN, James L.
                                                                                                                                                                    Sequence 23, Application US/08137800 Patent No. 5514774 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 51, Application US/08233788A
                                                                                                          Sequence 23, Application US/08137800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
ORGANISM: Conus ochroleucus
JENCE 42 AA; 4618 MW; 9505 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 28,957
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPA: 202-902 UNIVERSITION FOR SEQ ID NO: 23 SEQUENCE CHARACTERISTICS: "PUGTH: 42 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 23.8%;
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PLP-DCCRQKTCSCRLYEL 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,383
FLING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATPONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
                                                   42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 61; DB 1;
Pred. No. 5.85e+
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
                                                   PRT;
                                                                                                                                                                                                                                                                                 Sequence 23, Application US/08477383 Patent No. 5589340 GENERAL INFORMATION:
                                                                                                                                                                                                                              Sequence 23, Application US/08477383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
ORGANISM: Conus ochroleucus
JENCE 42 AA; 4618 MW; 9505 CN;
                                                   STANDARD;
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llarity 47.4%;
Conservative
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 PVPSDCCQVSSCW-NLYGL 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A. ZIP: 20005
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Best Local Similarity
                                                US-08-477-383-23
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US-08-137-800-23
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Gaps

42 AA.

PRT;

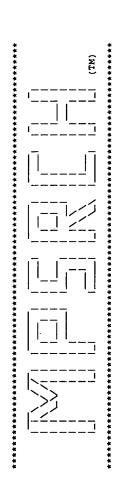
STANDARD;

RESULT

ä

SEQUENCE

Best Loca Matches



protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:19:34 1998; MasPar time 3.95 Seconds 128.266 Million cell updates/sec : 0

>US-08-938-548A-8 (1-33) from US08938548A.pep 256 ular output not generated. Title: Description: Perfect Score:

1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 PAM 150 Gap 11 Scoring table: Sequence:

124785 seqs, 15338987 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq31-2 Database:

1:paril 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part22 23:part25 26:part26 27:part27

Mean 22.991; Variance 84.736; scale 0.271 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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363											
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rmethyl-D-a xcitatory a caid receptor a caid receptor ge conotoxi gry cone sna illa enterit embrane ant equence.  gy protein a llergen Bl. pply polymenase III rez fusion venom pepti nal sequence web spider nal sequence of viper se of viper se of viper symbets aub beta sub beta sub protein.	Murine Lysti iong iso
R66039 R842054 R441054 R441054 W12745 W24890 W27333 W27333 R62758 W311950 W311950 W31950 W31950 W31950 W31950 W31969 R4244 R4244 R4244 R4244 R4244 R31005 R3	507
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### ALIGNMENTS

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DNA encoding porcine complement inhibitor - useful in porcine organ transplant to humans
Claim 3; Page 12-14; 20pp; Japanese.
This protein is a porcine complement inhibitor encoded by pMCPcDNA (761098). The DNA is useful for large scale production of recombinant porcine complement inhibitor, which is useful for porcine organ transplantation into humans. The DNA clone pMCPcDNA is also useful in the analysis of the promoter region of porcine complement inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                           24-SEP-1997 (first entry)
Porcine complement inhibitor.
porcine; pig; complement; inhibitor; organ transplantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 2
1898461 standard; Protein; 373 AA.
1898461: 25-826-1996 (first entry)
189461: Murine ICE-ced-3 homologue.
1896-2; murine ICE-ced-3 homologue; programmed cell death;
                                                                                                                                                                                                                                                                                                                                                                                                Score 77; DB 23; Length 363;
Pred. No. 6.26e+00;
7; Mismatches 9; Indels
                                                                                                                                                                                         Murakami H, Shigehisa T, Toyomura K;
WPI; 97-087378/08.
N-PSDB; T61098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; Protein; 363 AA.
                                                                                                                 09-JAN-1997.
19-JUN-1996; JD1704.
20-JUN-1995; JP-178254.
(NIME-) NIPPON MEAT PACKERS INC.
(NIHA-) NIPPON HAM KK.
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 30.1%;
Best Local Similarity 39.3%;
Matches 11; Conservative
                                                                      promoter
                                                                                                                                                                                                                                                                                                                                                                      363 AA;
                                                                                     Sus scrofa.
WO9700951-A1.
                                                                         analysis;
                                                                                                                                                                                                                                                                                                                                                                         Sequence
W12414 s
W12414;
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RESULT

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WPI; 97-087323/08.

WPI; 97-087323/08.

New agouti signal protein peptide(s) and nucleic acids - used for altering melanin prodn., for treating e.g. melasma photo-ageing spots, solar keratosis or vitiligo.

Taltering melanin prodn., for treating e.g. melasma photo-ageing spots, solar keratosis or vitiligo.

The sequences given in W10101-29 are biologically active peptides.

The sequences given in W10101-29 are useful for cosmetic purposes and fragments of the agouti signalling protein (ASP) which have depigmenting activity. These peptides are useful for cosmetic purposes and for cilinical application in the prevention or treatment of various hyperpigmentary conditions and diseases such as melasma photoageing spots, solar keratosis, and post-inflammatory hyperpigmentation such as occurs at sites of wound healing. They can also be used to provide enhanced eumelanogenesis for treating eg. vitiligo, leucoderma, some forms of albinism and hair greying.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-529-1997 (first entry)

Human agout1 signalling protein fragment #2.

Agout1 signalling protein; ASP; depigmenting activity; cosmetic;

hyperpigmentary condition; melasma photoageing spots; solar keratosis;

post-inflammatory hyperpigmentation; wound healing; eumelanogenesis;

vitiligo; leucoderma; albinism; hair greying.
                                                                                                                                DNA corresp. to (part of) foot and mouth disease virus RNA - useful in prepn. of vaccines for producing antibodies against the virus Example; Fig 6; 57pp; English.
The inventors claim a DNA molecule comprising a nucleotide sequence corresp. to all or a portion of foot-and-mouth disease virus RNA (FMDV). The DNA molecule is esp. for a precursor of FMDV capsid protein. It esp. codes for FMDV protein p88 and VPI-VP4. It may code for VH4, VP2, VP3 and VPI contiguously. The inventors also claim a vaccine for stiumlating prodn. of antibodies against FMDV in a mammal which comprises at least one of the above recombinant proteins produced by a host cell transformed with the DNA.
  (NATR ) National Res Dev Corp.
(WELL) Wellcome Foundation Ltd.
Boothroyd JC, Cross GAM, Highfield PE, Winther MD, Rowlands DJ,
Brown F, Harris TJK, Lowe PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 23; Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 65; DB 5; Length 78; Pred. No. 7.06e+01; 9; Mismatches 5; Indels
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Pred. No. 8.59e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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21-JUN-1995; U10695.
23-JUN-1995; US-000436.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 OKTCSCRLYELLHGAGNHAAGILT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LT 9
W10105 standard; protein; 45 AA.
W10105;
17-SEP-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W10106 standard; protein; 45 AA. W10106;
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Similarity 41.2%;
7; Conservative
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Best Local Similarity 37.5%;
Matches 9; Conservative
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                                                                                          WPI; 82-26702E/14.
N-PSDB; N20019.
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WO9700892-A2.
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congenital craniofacial and other skeletal or dental anomalies, induction of local endochondral bone formation in non-union fractures, peridontal applens. requiring bone formation and cartilage repair, eg in the treatment of osteoarthritis.

See also P95679-P95692 and N95097.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human mature uniding diphosphate galactose-4-epimerase (UDP-G4E) (W01619) catalyses a reversible reaction between UDP-glucose and UDP-galactose that allows galactose residues to enter into the main pathways of glucose metabolism. A deficiency of the enzyme results in galactosaemia. The amino acid sequence of UDP-G4E was deduced from a CDNA clone (T58301) derived from a human endometrial tumour library. Recombinant UDP-G4E polypeptides can be produced in transformed host (e.g. E. coli, COS, Sf9 insect) cells or expressed in vivo for use in the treatment of UDP-G4E deficiency, e.g.
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding human uridine diphosphate galactose-4-epimerase - used
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24-APR-1997 (first entry)
Human uridine diphosphate galactose-4-epimerase.
Uridine diphosphate galactose-4-epimerase; UDP-G4E; galactosaemia;
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Pred. No. 5.80e+01;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-AUG-1992 (first entry)
Sequence of a foot and mouth disease virus capsid protein encoded by a region of recombinant plasmid pFA61/t'6
Vaccine; antibody; capsid protein; immunogen; antigen; foot and mouth disease.
                                                                                                                                                            Score 66; DB 1; Length 102;
Pred. No. 5.80e+01;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in the treatment and diagnosis of galactosaemia Claim 1; Page 43-44; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                        JT 6
W01619 standard; Protein; 348 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.8%;
                                                                                                                                                               Query Match 25.8%;
Best Local Similarity 56.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                         34 cpyplyeilngs-nha 48
                                                                                                                                                                                                                                                                                                   12 CSCRLYELLHGAGNHA 27
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GB-034147.
GB-011064.
GB-025150.
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11-MAY-1995; U05785.
11-MAY-1995; WO-U05785.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy; diagnosis.
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WPI; 96-518666/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 AA;
                                                                                                                    102 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; T58301
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22-OCT-1980;
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17-SEP-1981.
                                                                                                                 Sequence
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Bacillus thuringlensis toxin gene - useful in recombinant hosts, particularly plants for the control of nematodes Claim 4; Page 35-39; 44pp; English.

This sequence represents the protein encoded by a polynucleotide of the invention. The polynucleotide of the invention is a sequence from a Bacillus thuringlensis (Bt) isolate selected from PS80JJ1, PS158D5, PS169E, PS177F1, PS177G, PS204G4 and PS204G6, that encodes a toxin active against nematodes. This sequence represents the 167P protein, and is a delta-endotoxin protein. The polynucleotides and toxins can be used for the control of nematode pests such as Panagrellus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New agout 1 signal protein peptide(s) and nucleic acids - used for altering melanin prodn., for treating e.g. melasma photo-ageing spots, solar keratosis or vitiligo claim 5; page 8-9; 67pp; English.

The sequences given in W10101-29 are biologically active peptides and fragments of the agouti signaling protein (ASP) which have depigmenting activity. These peptides are useful for cosmetic purposes and for clinical application in the prevention or treatment of various hyperpigmentary conditions and diseases such as melasma photoageing spots, solar keratosis, and post-inflammatory hyperpigmentation such as occurs at sites of wound healing. They can also be used to provide enhanced eumelanogenesis for treating eg. vitiligo, leucoderma, some
           Agouti signalling protein; ASP; depigmenting activity; cosmetic; hyperpigmentary condition; melasma photroageing spots; solar Keratosis; post-inflammatory hyperpigmentation; wound healing; eumelanogenesis; vitiligo; leucoderma; albinism; hair greying.
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Nematode toxin 167P protein.
PCR primer; amplify; nematode toxic protein; Bacillus thuringiensis; delta-endotoxin gene; nematode pest control; Panagrellus redivivus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 64; July 20. Pred. No. 8.59e+01;
                                                                                                                                                                                                                                                                                                                              /note= "Start of Cysteine-rich motif"
                                                                                                                                                                                                                                                                      "Start of basic region"
                                                                                                                                                                                    /note= "Signal sequence" 32
                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUN-1995; US-000436.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            forms of albinism and hair greying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein; 1167
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Best Local Similarity 41.2%;
Matches 7; Conservative
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Fu J, Narva KE, Payne J;
WPI; 97-480163/44.
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21-MAR-1997; U04755.
21-MAR-1996; US-590554.
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Bacillus thuringiensis.
WO9734926-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hearing VJ;
WPI; 97-087323/08.
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                                                                                                                          Mus musculus
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W31504 a
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The sequences given in W10101-29 are biologically active peptides and fragments of the agout1 signalling protein (ASP) which have depigmenting activity. These peptides are useful for cosmetic purposes and for clinical application in the prevention or treatment of various hyperplamentary conditions and diseases such as melasma photoageing spots, solar keratosis, and post-inflammatory hyperplamentation such as occurs at sites of wound healing. They can also be used to provide formation of the second of the second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         solar keratosis;
Example; Page 17; 28pp; English.

The sequence is that of a polypeptide present in fraction K of the venom of Agelenopsis aperta, it blocks calcium channels in cells of both mammals and invertebrates, partic. those affecting neuronal and muscle cells. It may be used in the treatment of angina, hypertension, cardiomyopathies, supraventricular arrhythmia, oesophogeal achalasia, premature labour, and Raynaud's disease. It may also be of use in the study of cell physiology and in the control of invertebrate pests. It may be produced synthetically.
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Human agouti signalling protein.

Agouti signalling protein, ASP; depigmenting activity; cosmetic;

hyperpigmentary condition; melasma photoageing spots; solar keratosi

post-inflammatory hyperpigmentation; wound healing; eumelanogenesis;

vitiligo; leucoderma; albinism; hair greying.
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Pred. No. 8.59e+01;
3; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                              Length 48;
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                                                                                                                                                                                                                                                                                                                           Score 64; DB 8; Lo
Pred. No. 8.59e+01;
2; Mismatches 4
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86
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23-JUN-1995; US-000436.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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W10102 standard; protein; 130 AA.
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W10101 standard; protein; 131 AA.
W10101;
17-SEP-1997 (first entry)
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Murine agouti signalling protein
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Best Local Similarity 45.5%;
Matches 5; Conservative
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Gaps

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

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Title:

>US-08-938-548A-6 (1-130) from US08938548A.pep 954 1 MNLPSTKVPWAAVTLLLLLL......GRRCPTATALAPRGGSRV 130 Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

140542 seqs, 42109429 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptrembl5
1:sp\_fungi 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_ahr 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified Database:

Mean 39.989; Variance 88.114; scale 0.454 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Pred.	3.56e-02	8.61e-02	3.65e-0	3.65e-0	1.95e+0	2.56e+0(	2.56e+0	2.56e+0	3.36e+0	4.40e+0	4.40e+0	4.40e+0	4.40e+0(	5.75e+0(	5.75e+0(	7.50e+00	7.50e+00	7.50e+00	7.50e+00	7.50e+00
Description	HYPOTHETICAL 74.6 KD P	PLATELET GLYCOPROTEIN	ACYLOXYACYL HYDROLASE.	FRIZZLED PROTEIN HOMOL	PROLINE- AND LEUCINE-R	LECITHIN: CHOLESTEROL A	CYCLOOXYGENASE 1.	CYCLOOXYGENASE ISOFORM	SORTILIN PRECURSOR.	COLIA1 AND PDGFB FUSIO	C-SIS PROTO-ONCOGENE (	LEUCINE ZIPPER WITH BA	PROSTAGLANDIN H SYNTHA	HYPOTHETICAL 23.1 KD P	TIGHT JUNCTION PROTEIN		POLYPROTEIN PRECURSOR	DNA BINDING PROTEIN E1	PROSTAGLANDIN ENDOPERO	SIMILARITY TO MOUSE SM
QI	023352	008770	035298	008463	041051	035849	063684	063921	099523	015186	015354	091640	062731	006319	095168	098708	041283	090491	015122	018780
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% Query Match Length DB	629	267	574	641	106	440	602	602	833	154	185	331	602	226	1174	225	271	583	599	1238
% Query Match	11.1	10.8	10.3	10.3	9.6	9.5	9.5	9.5	9.4	9.3	ъ. В.	9.3	9.3	9.5	9.5	9.1	9.1	9.1	9.1	9.1
Score	106	103	86	86	92	91	91	91	06	83	83	89	89	88	88	87	87	87	87	87
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٠.	MIN	POLYKETIDE	POLYKETIDE	COTE	INE	PUTATIVE	PUTATIVE	-DEP	NE	PRO	THYROID	H DE	THE	NE	YLG	8	MO1B2.2.	MYOMODULIN	FROM BASES	MYOMODULIN	FERREDOXIN	LASE	;	WLA	
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P9752	065813	030765	03076	015354	00283	000348	014768	083101	06047	043495	091654	035413	065568	060470	000542	015016	179	027916	P76081	907974	P77233	01702	P7240	0191	
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## ALIGNMENTS

								AE;				RYN N.,	RYN N.,	RYN N., A., JONES	RYN N., A., JONES SCHUELLER	RYN N., A., JONES	RYN N., A., JONES SCHUELLER	RYN N., A., JONES SCHUELLER	A., JONES SCHUELLER	RYN N., A., JONES SCHUELLER	RYN N., A., JONES SCHUELLER	RYN N., A., JONES SCHUELLER	A., JONES SCHUELLER	RYN N., A., JONES SCHUELLER	RYN N., A., JONES SCHUELLER
				<u></u>	ATE)			EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;				OHL T., TERF	SEQUENCE FROM N.A. BEVAN M., STIEKEMA W., MURPHY G., WAMBUTT R., POHL T., TERRYN N., KREIS M., KAVARAGH T., ENTTAN K.D., RIEGER M., JAMES R.,	OHL T., TERR JAMES R., DUESTERHOFT	OHL T., TERRYN N., JAMES R., DUESTERHOFT A., JONES MEWES H.W., SCHUELLER	OHL T., TERRYN N., JAMES R., DUESTERHOFT A., JONES MEWES H.W., SCHUELLER	DHL T., TERRIAMES R., DUESTERHOFT GEWES H.W., SANKS.	DHL T., TERR TAMES R., DUESTERHOFT GEWES H.W.,	DHL T., TERR JAMES R., JUESTERHOFT GEWES H.W., SANKS.	OHL T., TERR TAMES R., TEWES H.W., JEWES H.W.,	JHL T., TERR JAMES R., JUESTERHOFT GEWES H.W., SANKS.	OHL I., TERR TAMES R., UDESTERHOFT TEWES H.W., SANKS.	JHL T., TERR TAMES R., ULESTERHOFT MEWES H.W., SANKS.	JHL T., TERR TAMES R., UNESTERHOFT MEWES H.W., SANKS.	Y G., WAMBUTT R., POHL T., TERR N K.D., RIEGER M., JAMES R., P., OBERWAIER B., DUSSTERHOFT Y M., BANCROFT I., MEWES H.W., /GENBANK/DDBJ DATA BANKS. OJECT, ESSA; /GENBANK/DDBJ DATA BANKS. ; B301B713 CRC32; SCOFE 106; DB 8; Length 679;
	679 AA.			LAST SEQUENCE UPDATE)	LAST ANNOTATION UPDATE)			SPERMAE; DI				BUTT R., PC	BUTT R., PC IEGER M., J	BUTT R., PC IEGER M., J MAIER B., I	BUTT R., PC IEGER M., J MAIER B., I CROFT I., N	BUTT R., PC IEGER M., J MAIER B., I CROFT I., N	BEYAN M., STIEKEMA W., MURPHY G., WAMBUTT R., POHL T KREIS M., KAVANAGH T., ENTIAN K.D., RIEGER M., JAMES POUGDOMENBCH P., HATZOPOULOS P., OBERWAIER B., DUEST PRIME K., BANGORGE W., DELSENY M., BANCROFT I., MEWES CHALMATIS N.)	BUTT R., PC IEGER M., J MAIER B., D CROFT I., N	BUTT R., PC IEGER M., J MAIER B., E CROFT I., M DDBJ DATA E	BUTT R., PC IEGER M., J MAIER B., D CROFT I., M DDBJ DATA E	BUTT R., PC IEGER M., J MAIER B., D CROFT I., M DDBJ DATA E SA;	BEYAN M., STIEKEMA W., MURPHY G., WAMBUTT R., POHL T BEYAN M., STIEKEMA W., MURPHY G., WAMBUTT R., POHL T PUIGDOMENECH P., HATZOPOULOS P., OBERMAIER B., DUEST PALME K., ANGORGE W., DELSENY M., BANCROFT I., MEWES CHALMATZIS N.; SCHMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS SEQUENCE FROM N.A. SEQUENCE FROM N.A. SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS	BUTT R., PC IEGER M., J MAIER B., D CROFT I., M DDBJ DATA B SA;	, WAMBUTT R., PCD., RIEGER M., J . OBERMAIER B., D I., BANCROFT I., M .NBANK/DDBJ DATA E .CT, ESSA; .NBANK/DDBJ DATA E .NBANK/DDBJ DATA E	BUTT R., PC IEGER M., J MAIER B., D CROFT I., M DDBJ DATA E SA; DDBJ DATA E 13 CRC32; ; DB 8; I
	PRT; 6		CREATED)	LAST SEQUE		<u>.</u>	ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).	TA; ANGIO				IY G., WAME	IY G., WAME IN K.D., R.	BEYAN M., STIEKEMA W., MIRPHY G., WAMBUTT R., KREIS M., KAVANAGH T., EWITAN K.D., RIEGER M., THIGHOMENRCH P., HATZOPOULOS P., OBERWAIER B.,	BEYAN M., STIEKEMA W., MURPHY G., WAMBUTT R., KREIS M., KAYANAGH T., ENTIAN K.D., RIEGER M., PUIGDOMENECH P., HATZOPOULOS P., OBERWAIER B., PALME K., ANSORGE W., DELGENY M., BANCROFT I.,	BEVAN M., STIEKEMA W., MURPHY G., WAMBUTT R., I KREIS M., KAYANAGH T., ENTIAN K.D., RIEGER M., PUIGDOMENECH P., HATZOPOULOS P., OBERWAIER B., PALME K., ANSORGE W., DELSENY M., BANCROFT I., CHALMATZIS N.;	IY G., WAME IN K.D., RJ S.P., OBERA IY M., BANC JGENBANK/I	IY G., WAME IN K.D., RJ S.P., OBERA IY M., BANC	II G., WAME IN K.D., RJ S.P., OBERA IY M., BANC J/GENBANK/I	BEYAN M., STIEKEMA W., MURPHY G., WAMEUT KREIS M., KAVANAGH T., ENTIAN K.D., RIEG PUIGOMENBEH P., HATZOPOULOS P., OBERWAI PALME K., ANSORGE W., DELSENY M., BANCRO CHALWATIS N., SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDB [2] SEQUENCE FROM N.A.	IY G., WAME IN K.D., RI IN K.D., RI IY M., BENU I/GENBANK/I KOJECT, ESS I/GENBANK/I	IY G., WAME IN K.D., RI I P., OBERA IY M., BANG L/GENBANK/I	IY G., WAME IN K.D., RI IY M., BANC J./GENBANK./I ROJECT, ES:	IY G., WAME IN K.D., RJ IN K.D., RJ IN M., BANC JGENBANK IN KOJECT, ESS JGENBANK II 17, B301B71	IY G., WAME IM K.D., RJ IP M., DBENNE IY M., BANN JGENBANK/I KOJECT, ESS JGENBANK/I  SCOTE 106;
	PRELIMINARY;		05,	REL. 05,	05,	D PROTEIN	A (MOUSE-	EMBRYOPHY	RAE.			W., MURPH	W., MURPH T., ENTIA	W., MURPH T., ENTIA TZOPOULOS	W., MURPH T., ENTIA (TZOPOULOS	W., MURPH T., ENTIA TZOPOULOS ', DELSEN	W., MURPH T., ENTIA TZOPOULOS ', DELSEN ) TO EMBL	W., MURPH T., ENTIA TZOPOULOS '., DELSEN ) TO EMBL	W., MURPH T., ENTIA TZOPOULOS '., DELSEN ) TO EMBL	W., MURPH T., ENTIA TZOPOULOS T., DELSEN ) TO EMBL ) TO EMBL	W., MURPH T., ENTIA TZOPOULOS TZOPOULOS TO EMBL ) TO EMBL ) TO EMBL	W., MURPH T., ENTIA T., ENTIA T., DELSEN TO EMBL TO EMBL TO EMBL TO EMBL TO EMBL TO EMBL	W., MURPH T., ENTIA T.OPOULOS T. DELSEN ) TO EMBL ENCING PR D) TO EMBL 1 ) TO EMBL 1 ) TO EMBL	TIEREMA W., MURHY WANAGH T., ENTIAN H P., HATZOPOULOS P. NSORGE W., DELSENY UN1997) TO EMBL/G OM N.A. SIS SEQUENCING PROJ JUN.1997) TO EMBL/G T. F325841; T. PROTEIN. T. PROTEIN. T. PROTEIN. G79 AA; 74635 MW;	w., MURPH T., ENTIA T., DELSEN T., DELSEN ) TO EMBL ) TO EMBL ) TO EMBL 41; N. 74635 MW
	PREL		9 (TREMBLREL.			AL 74.6 K	S THALIAN	PLANTA;	CRUCIFE		ROM N.A.	STIEKEMA	STIEKEMA	STIEKEMA KAVANAGH	STIEKEMA KAVANAGH CH P., HA	STIEKEMA KAVANAGH CH P., HA ANSORGE W	STIEKEMA KAVANAGH CH P., HA ANSORGE W N.;	STIEKEMA KAVANAGH CH P., HA ANSORGE W N.;	STIEKEMA (AVANAGH 'CH P., HA'CH P., HA'CH W.; N.; (JUL-1997	STIEKEMA (AVANAGH 'CH P., HA' CH P., HA' ANSORGE W N.; (JUL-1997 ROM N.A.	STIEKEMA CAVANAGH CH P., HA ANSORGE W N.; (JUL-1997 ROM N.A. PSIS SEQU	STIEKEMA CAVANAGH SH P., HA NL; CJUL-1997 CJUL-1997 ROM N.A. PSIS SEQU (JJUS SEQU (JJUS SEQU (JJUS SEQU	STIEKEMA CAVANAGH ANSORGE W N.; (JUL-1997 ROM N.A. PSIS SEQU (JUN-1997) SAT, E3268	STIEKEMA CAVANAGH AN S., HA N.; (JUL-1997 COM N.A. PSIS SEQU (JUN-1997 CON-	STIEKEMA AN PONGH N.; JUL-1997 (JUL-1997 ROM N.A. PEIS SEQU (JUN-1997 37; B3268 AL PROTEI 679 AA;
er 55	23352	023352;	01-JAN-1998	01-JAN-1998	01-JAN-1998	HYPOTHETICAL 74.6 KD PROTEIN.	RABIDOPSIS	UKARYOTA;	CAPPARALES; CRUCIFERAE.	1]	SEQUENCE FROM N.A.	EVAN M., 5	EVAN M., S	EVAN M., S REIS M., P UIGDOMENEC	EVAN M., S REIS M., F UIGDOMENEC	BEVAN M., STIE KREIS M., KAVA PUIGDOMENECH P PALME K., ANSO CHALWATZIS N.,	EVAN M., S REIS M., F UIGDOMENEC ALME K., P HALWATZIS	EVAN M., S REIS M., F UIGDOMENEC ALME K., F HALWATZIS UBMITTED (	BEVAN M., STIEKEMA KREIS M., KAVANAGH PUIGDOMENECH P., H PALME K., ACNSEGE CHALWATZIS N.; SUBMITTED (JUL.199 [2]	REIS M., R REIS M., R UIGDOMENEC AALME K., R HALWATZIS CHAMITTED (2)	EVAN M., S TUGDOMENE UIGDOMENE ALME K., F SHALWATZIS UBMITTED ( EQUENCE FI EQUENCE FI	EVAN M., S REIS M., R REIS M., R OLGDOMENEC ALME K., P RALMATZIS CUBMITTED ( 2) EQUENCE FI CU ARABIDO ( CUBMITTED ( CUBMITTED ( COMMITTED	BEYAN M., STIEKEMA W., MU KREIS M., KAVANAGH T., EN FULGE K., ANSONGE W., DEL CHALWATZIS N.; SUBMITTED (UUL-1997) TO E [2] SEQUENCE FROM N.A EU ARABIDOPSIS SEQUENCING SUBMITTED (UNN-1997) TO E EU ARABIDOPSIS SEQUENCING SUBMITTED (UNN-1997) TO E ENBL: 293337; a228841; -	RETAN M., STIEKEMA W RREIS M., KAVANAGH PULDEN B., HATI PALME K., ANSORGE W. CHALWATZIS N.; SCUBMITTED (JUL-1997) [2] SEQUENCE FROM N.A. EUR ARABIDOPSIS SEQUE SUBMITTED (JUN-1997) EMBI, ZG7337; E32684 HYPOTHETICAL PROTEIN SEQUENCE 679 AA;	BEVAN M., STIEKEMA W., MUR KREIS M., KNVANAGH T., ENT PUIGDOMENECH P., HATZOPOUL PALME K., ANSORGE W., DELS CHALMATZIS N.; SUBMITTED (JUL-1997) TO EM [2] SEQUENCE FROM N.A. ED ARABIDOPSIS SEQUENCING SUBMITTED (JUN-1997) TO EM EMBL; 297337; E326841; HYPOTHETICAL PROTEIN. SEQUENCE 679 AA; 74635 QUENTY MATCh 11.1%;
RESULT	o G			DI		DE	OS				RP S														anc.

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RESULT 2 PRELIMINARY; PRT; 567 AA.

1D 008770, AC 008770; PREMBLREL. 04, CREATED)

DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)

655 SP 656 :: 101 GA 102

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Gaps

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7; Mismatches 15; Indels

Score 91; DB 10; Pred. No. 2.56e+00;

4EBDC921 CRC32;

Length 602

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1 MSRRSLSLQFPLLLLLLLPPPPVLLTDAGVPSPVIP-CC 39
          ARCH. BIOCHEM. BIOPHYS. 307:361-368(1993).
EMBL; S67721; G460556; -.
                                                                                                                      602 AA; 69158 MW;
                                                                                                                                                                                    Query Match 9.5%;
Best Local Similarity 40.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SORTILIN PRECURSOR
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SEQUENCE
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O 01-MAY-1

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DT 01-MAY-1

OC 01-JAN-1

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                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SPRAGUE-DAWLEY AND WISTAR; TISSUE-LIVER;
WANG J., ANDERSON R.A., PARKS J.S.;
SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + STEROL = STEROL ESTER +
1-ACYLGLYCEROPHOSPHOCHOLINE.
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01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
CYCLOOXYGENASE ISOFORM COX-1 (FRAGMENT).
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RATTUS NORVEGICUS (RAT).
EUKRAYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYCLOOXIGENASE 1.
RATIUS NORYEGICUS (RAI).
EUKARYOTA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA
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STRAIN-FISHER 344;

STRAIN-FISHER 344;

FENG L., SUN W., XIA Y., TANG W.W., CHANNUGAM P., SOYOOLA E.,

WILSON C.B., HWANG D.;

WARCH. BICCHEM. BIOPHYS. 307:0-0(0).

EMBL: U03388; G415588; -.

SEQUENCE 602 AA; 69115 MW; DC2236E9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 94099619.
FENG L., SUN W., XIA Y., TANG W.W., CHANMUGAM P., SOYOOLA E.
WILSON C.B., HWANG D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 440;
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Pred. No. 2.56e+00;
7; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 91; DB 10; Length 44C
Pred. No. 2.56e+00;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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BIOCHIM. BIOPHYS. ACTA 1346:207-211(1997).
                                                                                                                                                                                    STRAIN-SPRAGUE-DAWLEY AND WISTAR; TISSUE-LIVER;
MEDLINE; 97363611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U62803; G2306762; -.
PROSITE; PS00120; LIPASE_SER; 1.
SANANGERASE; ACYLTRANGERASE.
SEQUENCE 440 AA; 49882 NW; 6CC16087 CRC32;
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01-NOV-1996 (TREMBLREL. 01, CR
01-NOV-1996 (TREMBLREL. 01, LA
01-NOV-1996 (TREMBLREL. 01, LA
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Best Local Similarity 62.5%;
Matches 15; Conservative
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Best Local Similarity 40.0%;
Matches 16; Conservative
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                                                                                                                                                  SEQUENCE FROM N.A
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EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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EUTHERIA; PRIMATES.
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                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
PETERSEN C.M., NIELSEN M.S., JACOBSEN L., TOMMERUP N., HOLM I ROIGAARD H., GLIEMANN J., MADSEN P., MOESTRUP S.K.;
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X98248; E246784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                 01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ė
69 LQRLLHGDPGEEDGAELDLNMTRSHSGGELESLA-RGRR 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.3%; Score 89; DB 2; L. Best Local Similarity 43.6%; Pred. No. 4.40e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 90; DB 2; I
Pred. No. 3.36e+00;
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015186;
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01-378-1998 (TREMBLREL. 05, CREATED)
01-378-1998 (TREMBLREL. 05, LAST SEQUENCE UPDAT
01-378-1998 (TREMBLREL. 05, LAST SEQUENCE UPDAT
01-378-1398 (TREMBLREL. 05, LAST SEQUENCE UPDAT
COLLAIA NND POGEB FUSION TRANSCRIPT (FRAGMENT).
HOMO SAPIENS (HUMAN).
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DZE351B9 CRC32;
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                                                                                                      833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: :: ||||| ||||: || :|| || || 10 WA-AVTLILLL-LLPPALLSLG-VDAQPLP 36
                                                                                                         PRT;
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34 833 S
833 AA; 92408 MW;
                                                                                                      PRELIMINARY;
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Best Local Similarity 53.3%;
Matches 16; Conservative
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SUBMITTED (SEP-1997) TO
EMBL; Y08643; E293780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154
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J. CELL BIOL. 124:949-961(1994).

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RX MEDLINE; 96421547.

RA BEATCH M., JESAITIS L.A., GALLIN W., GOODENOUGH D.A.,
RA STEVENSON B.R.;
RL J. BIOL. CHEM. 271:25723-25726(1996).

RN [3]
RN [4]
RA GOODENOUGH D.A.;
RA GOODENOUGH D.A.;
RA GOODENOUGH D.A.;
RA GOODENOUGH D.A.;
RA BEATCH M.;
RA BE
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Search completed: Thu Jul 30 09:18:04 1998 Job time: 41 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:16:51 1998; MasPar time 5.05 Seconds 646.000 Million cell updates/sec lar output not generated. :uo

>US-08-938-548A-6 (1-130) from US08938548A.pep 954 Description: Perfect Score: Sequence: Title:

1 MNLPSTKVPWAAVTLLLLLL......GRRCPTATATALAPRGGSRV 130

69111 seqs, 25083644 residues PAM 150 Gap 11 Searched:

Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

swiss-prot35 1:swiss1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 41.891; Variance 75.823; scale 0.552

#### SUMMARIES

Pred. No.	1.78e-02	9.43e-02	9.43e-02	9.43e-02	9.43e-02	9.43e-02	2.50e-01	2.50e-01	4.74e-01	4.74e-01	4.74e-01	8.89e-01	8.89e-01	1.21e+00	1.21e+00	1.21e+00	1.65e+00	2.24e+00	2.24e+00	2.24e+00	2.24e+00	2.24e+00	2.24e+00
Description	SECRETIN PRECURSOR (FR	PHOSPHATIDYLCHOLINE-ST	FIBULIN-1, ISOFORM A P	FIBULIN-1, ISOFORM B P	FIBULIN-1, ISOFORM C P	FIBULIN-1, ISOFORM D P	FIBRIL-FORMING COLLAGE	ATRIAL NATRIURETIC PEP	COMPLEMENT C1Q SUBCOMP	PHOSPHATIDYLCHOLINE-ST	PHOSPHATIDYLCHOLINE-ST	PLATELET-DERIVED GROWT	SALIVARY PROLINE-RICH	INFECTED CELL PROTEIN	4-1BB LIGAND (4-1BBL).	SEC14 CYTOSOLIC FACTOR	PDGF-RELATED TRANSFORM	INFECTED CELL PROTEIN	HYPOTHETICAL PROTEIN H	FERRIC ENTEROBACTIN TR	PHOSPHATIDYLCHOLINE-ST	RETINAL GUANYLYL CYCLA	COMPLEMENT C3 PRECURSO
A	SECR_PIG	LCAT_MOUSE	FBLA_HUMAN	FBLB_HUMAN	FBLC_HUMAN	FBLD_HUMAN	CAFF_RIFPA	ANPA_HUMAN	C10B_HUMAN	LCAT_RAT	LCAT_HUMAN	PDGB_HUMAN	PRP1_HUMAN	ICP3_HSV1D	41BL_HUMAN	SC14_YARLI	TSIS_SMSAV	ICP3_HSV1N	YCEC_HAEIN	FEPD_ECOLI	LCAT_PAPAN	CYGD_HUMAN	CO3_RAT
DB	Н	Н	Н	Н	7	-	Н	Н	-	-	Н	Н	Н	Н	Н	Н	ч	ч	-	Н	Н	ч	Н
& Query Match Length	131	438	266	601	683	703	1027	1061	251	440	440	241	331	252	254	497	226	245	322	334	440	1103	1663
& Query Match	10.6	10.1	10.1	10.1	10.1	10.1	9.7	9.7	9.5	9.5	9.5	9.3	9.3	9.5	9.5	9.5	9.1	9.0	9.0	9.0	0.6	0.6	9.0
Score	101	96	96	96	96	96	93	93	91	91	91	83	83	88	88	88	87	98	98	98	98	86	. 86
Result		7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

[6]
SEQUENCE OF 30-56.
SPECIES-C.PORCELLUS;
MEDLINE; 90254163.
BUSCAIL L., CAUVIN A., GOURLET P., GOSSEN D., DE NEEF P., RATHE J.,

3.03e+00	3.03e+00	3.03e+00	3.03e+00	4.09e+00	4.09e+00	4.09e+00	4.09e+00	4.09e+00	4.09e+00	4.09e+00	4.09e+00	5.50e+00	5.50e+00	5.50e+00	5.50e+00	5.50e+00	5.50e+00	5.50e+00	5.50e+00	5.50e+00	7.38e+00
PLACENTAL LACTOGEN I P	PLATELET - DERIVED GROWT	HYPOTHETICAL 28 KD PRO	LIPASE 1 PRECURSOR (EC	LYSIS PROTEIN.	E PROTEIN.	EPHRIN-A3 PRECURSOR (E	LIPASE 3 PRECURSOR (EC	HYPOTHETICAL 36.0 KD P	GIPASE ACTIVATING PROT	LUTROPIN-CHORIOGONADOT	PROTEIN-TYROSINE PHOSP	PLATELET GLYCOPROTEIN	OXALATE OXIDASE PRECUR	SL CYTOKINE PRECURSOR	PUTRESCINE TRANSPORT S	PHOSPHATIDYLCHOLINE-ST	HYPOTHETICAL 59.6 KD P	SERUM ALBUMIN PRECURSO	PROTEIN-TYROSINE PHOSP	ANGIOTENSIN-CONVERTING	GUANYLYL CYCLASE GC-E
PLC1_BOVIN	PDGB_MOUSE	YPE1_RHORU	LIP1_PSYIM	VGE_BPPHX	VGE_BPS13	EFA3_HUMAN	LIP3_MORSP	YCEC_ECOLI	RN_DROME	LSHR_PIG	PTPX_MOUSE	GPBB_PAPCY	OXO2_HORVU	FL3L_HUMAN	POTI_ECOLI	LCAT_RABIT	YABK_ECOLI	ALBU_CHICK	PTPX_RAT	ACE_RABIT	CYGE_MOUSE
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236	241	. 255	317	90	96	238	315	319	384	969	1001	208	224	235	281	440	536	615	1004	1310	1108
8.9	6.8	æ 6.	8.9	8.8	8.8	8.8	8.8	ω .ω	8.8	8. 8.	8.8	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	9.8
85	82	82	85	84	84	84	84	84	84	84	84	83	83	83	83	83	83	83	83	83	83
24	22	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

RESULT ID AC DT DT D	SECR. PIG STANDARD; PRT; 131 AA.   SECR. PIG STANDARD; PRT; 131 AA.   P01279;   L01779;   L01779;   L01779;   L01779;   L01777990 (REL. 14, LAST SEQUENCE UPDATE)   SECRETIN PRECURSOR (FRAGMENT).   SECR.   L01777999 (FRAGMENT).   SCR.   L01777999   L01777999   L017779999999999999999999999999999999999
8888	SUS SCROPA (PIG), BOS TAURUS (BOVINE), AND CAVIA PORCELLUS (GUINEA PIG). EUKRRYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; ARTIODACTYLA.
R R R R B	L1) SEQUENCE FROM N.A. SPECIES-PIG; MEDLINE; 90192795. KOPIN A.S., WHEELER M.B., LEITER A.B.; PROC. NATL. ACAD. SCI. U.S.A. 87:2299-2303(1990).
E E E E E	SEQUENCE OF 30-56. SPECIES-PIG; MEDLINE; 70282334. MUTI V., JORPES J.E., MAGNUSSON S.; EUR. J. BIOCHEM. 15:513-519(1970).
R R R R R R R R R R	SEQUENCE OF 30-59 AND 92-131. SPECIES-PIG; MEDLINE; 90370867. GAFYELIN G., JOERNVALL H., MUTT V.; PROC. NATL. ACAD. SCI. U.S.A. 87:6781-6785(1990).
R R R R R	SYNTHESIS OF 30-131. SPECIES-PIG; BODANSZKY M., ONDETTI M.A., LEVINE S.D., NARAYANAN V.L., SALTZA M.V., SHEEHAN J.T., WILLIAMS N.J., SABO E.F.; CHEM. IND. 1757-1758(1966).
8 K K K K	SEQUENCE OF 30-56. SPECIES-BOVINE; MEDLINE; 81237102. CARLQUIST M., JOERNVALL H., MUTT V.; FES LETT. 127:71-74(1981).
R R R R	SEQUENCE OF 30-56. SPECIES-C.PORCELLUS; MEDLINE; 90254163. BUSCAIL L., CAUVIN A., GOURLET P., GOSSEN D., DE NEEF P., RATHE J.,

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RN [2]

RP SEQUENCE OF 30-44.

RX MEDLINE; 993-5451.

RX MEDLINE; 993-5451.

REDINE; 993-5451.

REDINE; 993-5451.

REDINE; 993-5451.

REDINE; 993-5451.

REDINE; 993-5451.

C. --- SIMCELLIGAR LOCATION: EXTRACELLULAR MATRIX.

C. --- SIMCELLULAR LOCATION: EXTRACELLULAR MATRIX.

C. --- SIMCELLULAR LOCATION: EXTRACELLULAR MATRIX.

C. --- SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.

C. --- SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.

C. --- SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.

C. --- SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.

C. --- SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.

DR PRESS 6 A32826.

DR PIR; 936346; 936346.

DR PROSITE; PSOU1017; ANAPHYLATOXIN-L; 3.

PROSITE; PSOU107; ANAPHYLATOXIN-L; 3.

REDING ATTERNATIVE SPLICING; GLYCOPROTEIN; EXTRACELLULAR MATRIX; MAT
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3 X ANNPHYLATOXIN REPEATS.
ANAPHYLATOXIN-LIKE 1.
ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 3.
EGF-LIKE 2, CALCIUM-BINDING (EGF-LIKE 4, CALCIUM-BINDING (EGF-LIKE 5, CALCIUM-BINDING (EGF-LIKE 7, CALCIUM-BINDING (EGF-LIKE 7, CALCIUM-BINDING (EGF-LIKE 9, CALCIUM-BIN
      ARGRAVES W.S., TRAN H., BURGESS W.H., DICKERSON K.;
J. CELL BIOL. 111:3155-3164(1990).
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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. No. 9.43e-02;
Mismatches 8;
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                                                           01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
FIBRIL-FORMING COLLAGEN ALPHA CHAIN.
RIFTIA PACHYPTILA (TUBE WORM).
EUKARYOTA, METAZOA; VESTIMENTIFERA.
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                         PROSITE; PS00101; ASX_HYDROXIL; 4.
PROSITE; PS00102; EGE_1; FALSE_NEG.
PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
PROSITE; PS01188; ANAPHYLATOXIN_2; 3.
PROSITE; PS01187; EGE_2; 3.
PROSITE; PS01187; EGE_2; 8.
SIGNAL; ALTERNATIVE SPLICING; GLYCOPROTEIN; EXTRACELLULAR MATRIX;
REPERT; PLASMA; EGF-LIKE DOMAIN; CALCIUM-BINDING.
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Pred. No. 9.43e-02;
3; Mismatches 8; Indels
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3 X ANAPHYLATOXIN REPEATS.
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EGF-LIKE 2.
EGF-LIKE 3.
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MEDLINE; 90384859.
MERCHIG G., MALGARETI N., MAGNAGHI P., TARAMELLI R.;
MUCLEIC ACIDS RES. 18:5308-5308(1990).
-!- FUNCTION: CENTRAL ENZYME IN THE EXTRACELLULAR METABOLISM OF PLASMA LIPOPROTEINS. AMONG OTHER SUBSTRACTES IT ESTERFIES THE FREE CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS.
-!- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + STEROL - STEROL ESTER + 1.ACYLGHICEROPHOSPHOCHOLINE (PALMITOYL, OLEOYL, AND LINOLEOYL CAN BE TRANSFERRED; A NUMBER OF STEROLS, INCLUDING CHOLESTEROL, CAN ACT AS ACCEPTOR).
-!- ENTYRE REGULATION: APOLIPOPROTEIN A-I IS A POTENT ACTIVATOR FOR
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LINGJAL, LIPOPROTEIN, BACTERIAL, ETC.).

PIR: S11214; XXRTN.

PROSITE; PS00120; LIPASE_SER; 1.

TRANSFERASE; ACYLTRANSFERASE; LIPID METABOLISM; GLYCOPROTEIN; SIGNAL.

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01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-UJU-1993 (REL. 26, LAST ANNOTATION UPDATE)
PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
(LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE))
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 251;
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6; Mismatches 1; Indels
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Q -> E (IN REF. 2).
N -> D (IN REF. 2).
G -> P (IN REF. 2 A).
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Matches 8; Conser
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P18424;
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ACT SITE
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PHILOS. TRANS. R. SOC. LOND., B, BIOL. SCI. 306:345-354(1984).
-!- FUNCTION: C1Q ASSOCIATES WITH THE PROENZYMES CIR AND C1S TO YIELD C1, THE FIRST COMPONENT OF THE PROENZYMES CIR AND C1S TO YIELD COLLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE CA(2+)-DEPENDENT C1R(2)C1S(2) PROENZYME COMPLEX. AND EFFICIENT ACTIVATION OF C1 TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE FC REGIONS OF IGG ANTIDODY PRESENT IN IMMUNE COMPLEXES.
-!- SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEXES.
RAND SIN THE MODAR RATION OF 1:2:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: CLO SUBCOMPONENT IS COMPOSED OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE A & B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE C CHAIN.
-!- SIMILARITY: CONTAINS A CLO DOMAIN.
EMBL; X03084; G573114; --
EMBL; M36278; G179638; --
PIR; A03206; C18UQB.
PIR; B23422; B23422.
MIM; 120570; --
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01113; C1Q; 1. COMPLEMENT PATHWAY; PLASMA; HYDROXYLATION; GLYCOPROTEIN; COLLAGEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C10.
PYRROLIDONE CARBOXYLIC ACID.
INTERCHAIN (WITH CXS-26 IN CHAIN A).
                                                                                                                                                                                                                                                                                                                                                                         HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                               ;
Length 1061;
                                             10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENT C1Q, B CHAIN. COLLAGEN-LIKE.
                                                                                                                                                                                                                                                              21-JUL-1986 (REL. 01, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
COMPLEMENT CLQ SUBCOMPONENT, B CHAIN PRECURSOR.
Score 93; DB 1; L
Pred. No. 2.50e-01;
6; Mismatches 10
                                                                                                             251 AA
                                                                                      1 MPGPRRPAGSRIRLILLILLPPLILLLRGSHAGNL 35
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BIOCHEM. J. 203:559-569(1982).
                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 86076906.
REID K.B.M.;
BIOCHEM. J. 231:729-735(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIOCHEM. J. 179:367-371(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 79041552.
REID K.B.M., THOMPSON E.O.P.;
BIOCHEM. J. 173:863-868(1978)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 224-251 FROM N.A.
Query Match 9.7%;
Best Local Similarity 48.6%;
Matches 17; Conservative
                                                                                                                                                                                                                     STANDARD;
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MEDLINE; 82283890.
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MEDLINE; 80020137.
REID K.B.M.;
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MEDLINE; 85038855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT; SIGNAL
                                                                                                                                                                                                                     C1QB_HUMAN
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DISULFID
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D'ARCY A., WINKLER F.K., EGGIMANN B., HOSANG M.;
EMBO J. 11:3921-3926(1992).

-! FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR CELLS OF MESENCHMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS AFFINITY RECEPPOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
-! SUBBUILT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A AND B) CHAINS. HOMODIMER OF A AND B CHAINS ARE IMPLICATED IN TRANSFORMATION PROCESSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE PDGF RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 82-112.
MEDLINE; 83244981.
WATERFIELD M.D., SCRACE G.T., WHITTLE N., STROOBANT P., JOHNSSON A., WASTESON A., WESTERMARK B., HELDIN C.H., HUANG J.S., DEUEL T.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUTAGENESIS, IMPORTANCE OF ARG-108 AND ILE-111 FOR RECEPTOR-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 92097530.
CLEMENTS J.M., BAWDEN L.J., BLOXIDGE R.E., CATLIN G., COOK A.L.,
CRAIG S., DRUMMOND A.H., EDWARDS R.M., FALLON A., GREEN D.R.,
HELLEWELL P.G., KIRWIN P.M., NAYEE P.D., RICHARDSON S.J., BROWN D.,
EMBO J. 10:4113-4120(1991).
                                        RAO C.D., IGARASHI H., CHIU I.-M., ROBBINS K.C., AARONSON S.A.;
PROC. NATL. ACAD. SCI. U.S.A. 83:2392-2396(1986).
                                                                                                                                                                                                                                                                                                                                               RATNER L., JOSEPHS S.F., JARRETT R., REITZ M.S., WONG-STAAL F.;
NUCLEIC ACIDS RES. 13:5007-5018(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                        RAO C.D., IGARASHI H., PECH M.W., ROBBINS K.C., AARONSON S.A.;
COLD SPRING HARB. SYMP. QUANT. BIOL. 51:959-966(1986).
                                                                                                                                   CHIU I.-M., REDDY E.P., GIVOL D., ROBBINS K.C., TRONICK S.R.,
                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE, 85296313.
COLLINS T., GINSBURG D., BOSS J.M., ORKIN S.H., POBER J.S.;
NATURE 316:748-750(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BURGESS J., ODELL C.;
SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         İNTERCHAIN DISULFIDE BONDS.
MEDLINE; 92283833.
ANDERSSON M., OSSTMAN A., BAECKTROEM G., HELLMAN U.,
GEORGE-NASCIMENTO C., WESTERMARK B., HELDIN C.-H.;
J. BIOL. CHEM. 267:11260-11266(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEICH H.A., SEBALD W., SCHAIRER H.U., HOPPE J.; FEBS LEIT. 198:344-348(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [13]
X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTONIADES H.N., HUNKAPILLER M.W.;
SCIENCE 220:963-965(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 26-241 FROM N.A. MEDLINE; 86164981.
                                                                                               SEQUENCE OF 22-241 FROM N.A.
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                                                                                                                                                     AARONSON S.A.;
CELL 37:123-129(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 82-110.
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     SEQUENCE FROM N.A.
MEDLINE; 86205961.
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                                                                                                                                                                  PROSITE; PS00120; LIPASE SER; 1.
TRANSFERASE; ACYLTRANSFERASE; LIPID METABOLISM; GLYCOPROTEIN; SIGNAL;
POLYMORPHISM; DISEASE MUTATION.
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LCAT DEFICIENCY).
FISH-EXE DISEASE).
LCAT DEFICIENCY; PARTIALLY
                                                                                                                                                                                                                                                LECITHIN-CHOLESTEROL ACYLITRANSFERASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
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01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PLATELET-DERIVED GROWTH FACTOR, B CHAIN PRECURSOR (PDGF B-CHAIN)
PROPERTY OF A CONTROL OF THE PACTOR (PDGF B-CHAIN)
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MEDILINE: 84250225.
JOSEPHS S.F., RAINER L., CLARKE M.F., WESTIN E.H., REITZ M.S.,
WONG-STAAL F.;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FISH-EYE DISEASE) ICAT DEFICIENCY).
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-> M (IN FISH-EXE DISEASE)
-> H (IN REF. 3).
69727CDF CRC32;
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DEFECTIVE ENZYME).
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21-JUL-1986 (REL. 01, LAST SEQI
01-NOV-1997 (REL. 35, LAST ANNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49578 MW;
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Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCIENCE 225:636-639(1984).
M26268; G187025; -. X04981; G34287; -. M17959; G386858; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345
371
257
                                                        PIR, A00571; XXHUN.
PIR; A29661; A29661.
PIR; A25575; A25575.
PIR; JQ0036; JQ0036.
MIM; 136120;
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371
257
440 AA;
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P01127;
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VARIANT CONFLICT SEQUENCE

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Query Match

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CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUR. J. IMMUNOL. 24:2219-2227(1994).
-!- FUNCTION: INDICES THE PROLIFERATION OF ACTIVATED PERIPHERAL BLOOD
T CELLS. MAY HAVE A ROLE IN ACTIVATION-INDUCED CELL DEATH (AICD).
MAY PLAY A ROLE IN COGNATE INTERACTIONS BETWEEN T CELLS AND
121 HPPSRPFRLPPRLALRLRVTAEHLA-RLRL-RRAGGEGAPEPPATPATPATPATPAT 178
                            ); 94374434.
N. R., SMITH C.A., TOUGH T.W., DAVIS-SMITH T., ARMITAGE R.J., N. RODY E., BAKER E., SUTHERLAND G.R., DIN W.S., GOODWIN R.G.; INMUNOL. 24:2219-2227(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBUNTT: HOMOTRIMER (POTENTIAL).
-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
-1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, PLACENTA, LUNG, SKELETAL MUSCLE AND KIDNEY.
-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                            01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
4-1BB LIGAND (4-1BBL).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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PROSITE; PS50049; TNF 2; 1.
CYTOKINE; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 88; DB 1; Le
Pred. No. 1.21e+00;
4; Mismatches 1
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C68C1B27 CRC32;
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26624 MW;
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Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                      STANDARD;
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127 GSRV 130
                                                                                           179 PARV 182
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P41273;
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27 LPWALVAGLILLILLAAA 44 :||| |: |||||||: || 8 VPWAAVT-LLLLLLEPPA 24

Search completed: Thu Jul 30 09:17:05 1998 Job time: 14 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:16:01 1998; MasPar time 7.56 Seconds 628.387 Million cell updates/sec : uo un:

ular output not generated. Title:

>US-08-938-548A-6 (1-130) from USO8938548A.pep 954 1 MNLPSIKVPWAAVTLLLLLL......GRRCPTATATALAPRGGSRV 130

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

120441 seqs, 36531193 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d Database:

Mean 39.951; Variance 87.022; scale 0.459 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		dР					
Result No.	Score	Query Match	Length DB	DB	Ð	Description	Pred. No.
	101	10.6	131		SEPG	secretin precursor -	1.146-01
100	100	10.5	495	(7)	JA0091	catalase (EC 1.11.1.6	1.52e-01
e	98	10.3	641	~	A45054		2.72e-01
4	96	10.1	438	Н	XXMSN	phosphatidylcholine	4.82e-01
เว	96	10.1	601	~	B36346	fibulin 1 precursor,	4.82e-01
9	96	10.1	683	7	C36346	fibulin 1 precursor,	4.82e-01
7	93	9.7	1027	7	S28774	collagen alpha chain	1.12e+00
<b>&amp;</b>	. 93	9.7	1061	~	OYHUAR	natriuretic peptide r	1.12e+00
6	91	9.5	253	-	CIHUQB	complement subcompone	1.96e+00
10	91	9.5	440	Н	XXRTN	phosphatidylcholine	1.96e+00
11	91	9.5	440	Н	XXHUN	phosphatidylcholine	1.96e+00
12	91	9.5	602	7	S39782	cyclooxygenase 1 - ra	1.96e+00
13	89	9.3	185	~	S58383	hypothetical protein	3.38e+00
14	88	9.3	230	7	A55030	platelet-derived grow	3.38e+00
15	88	9.3	241	ч	PFHUG2	platelet-derived grow	3.38e+00
. 16	83	9.3	392	-	PIHUB6	salivary proline-rich	3.38e+00
17	88	9.3	602	7	869198	prostaglandin G/H syn	3.38e+00
18	88	9.5	245	7	S43293	FLT3/FLK2 ligand (clo	4.43e+00
19	88	9.5	491	7	JC6197	stromelysin 3 (EC 3.4	4.43e+00
20	88	9.5	497	7	S43745	phosphatidylinositol-	4.43e+00
21	87	9.1	226	Н	TVMVSS	PDGF-related transfor	5.79e+00
22	87	9.1	271	~	A25669	PDGF-related transfor	5.79e+00
23	87	9.1	583	7	150518	DNA binding protein E	5.79e+00

79e+00	56e+00	56e+00	56e+00	56e+00	56e+00	85e+00	85e+00	85e+00	85e+00	85e+00	85e+00	28e+01	.28e+01	28e+01							
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prostaglandin-endoper	hypothetical protein	ferric enterobactin t	phosphatidylcholine	guanylate cyclase (EC	complement C3 precurs	placental lactogen pr	platelet-derived grow	hypothetical protein	triacylglycerol lipas	_	endothelin receptor t	gene E protein - phag	protein 108 precursor	triacylglycerol lipas	lutropin-choriogonado	lutropin-choriogonado	NADH dehydrogenase (u	GTPase-activating pro	GTPase-activating pro	lutropin-choriogonado	hypothetical protein
A36746	G64151	S16296	JC1502	JH0717	C3RT	A37930	PFMSGB	S12255	S28225	S57275	JC5501	JS0455	S26409	S14276	D41344	C41344	S68129	B48122	A48122	A41344	S61239
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599	322	334	440	1102	1663	236	241	255	317	317	613	91	102	315	329	331	342	383	384	969	701
9.1	0.6	9.0	0.6	9.0	9.0	ۍ. ه	8.9	6.8	6.8	8.9	ω σ.	8.8	8.8	ω	8.8	8.8	8.8	89.		ω. 8.	8.8
87	86	86	86	86	86	82	82	82	82	82	82	84	84	84	84	84	84	84	84	84	84
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

SEPG #type complete secretin precursor - pig #formal_name Sus scrofa domestica #common_name domestic pig 24.Apr-1984 #sequence_revision 12.Apr-1996 #text_change 70.war-1998	ESSIONS B35094; A01544; A36052 ERENCE A35094 #authors Kopin, A.S.; Wheeler, M.B.; Leiter, A.B. #journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2299-2303 #title Secretin: structure of the precursor and tissue distribution of the mRNA. #cross_references MUID:90192795	ferenc ferenc A9114 Mutt, Eur. Struc nces M A0154	##residues 30-56 ##label MUT ##note tryptic peptides were sequenced ERENCE A36052 #authors Gafvelin, G.; Joernvall, H.; Mutt, V. #journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6781-6785 #title Processing of prosecretin: isolation of a secretin precursor from porcine intestine. #cross.references MuiD:90370867 #accession A36052 ##status preliminary ##molecule_type protein ##status 30-59, R', 92-131 ##label GAF	A90016 A90016 Bodanszky, M.; Ondetti, M.A.; Levine, S.D.; Narayanan, V.L.; Salcza, M.V.; Sheehan, J.T.; Williams, N.J.; Sabo, E.F. Chem. Ind. (1966) :1757-1758 Synthesis of a heptacosapetide amide with the hormonal activity of secretin. annotation synthesis confirmed the proposed structure of the natural hormone #superfamily glucagon amidated carboxyl end; duodenal mucosa; duplication; hormone;
RESULT 1 ENTRY TITLE ORGANISM DATE	ACCESSIONS REFERENCE #authors #journal #fitle	## ## ## ## ## ## ## ## ## ## ## ## ##	##residues ##note REFERENCE #authors #journal #fille #cross-refere #accession ##status ##status ##status ##status ##status ##status	REFERENCE #authors #journal #title #contents #note CLASSIFICATION KEYWORDS

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#submission
#description
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Fibulin, a novel protein that interacts with the fibronectil receptor beta-subunit cytoplasmic domain.
                                                                                            #authors Argraves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K.
#journal J. Cell Biol. (1990) 111:3155-3164
#title Fibulin is an extracellular matrix and plasma glycoprotein
#cross-references MUD:91100426
#accession B36346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors Argraves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K.
#journal J. Cell Biol. (1990) 111:3155-3164
#title Fibulin is an extracellular matrix and plasma glycoprotein
with repeated domain structure.
#cross-references WUID:91100426
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#product fibulin 1 splice form C #status predicted
#label MAT\
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predicted
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#formal_name Homo sapiens #common_name man
19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change
29-Aug-1997
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19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change
10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fibulin 1 precursor, splice form C - human fibulin C fibulin 1 splice form A; fibulin 1 splice form
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type mRNA
##residues_1-566 ##label AR2
##cross-references GB:X53741; NID:g31414; PID:g31415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues 1-683 ##label ARG
##cross-references GB:X53743; NID:931418; PID:931419
                                                                                                                                                                                                                                                                                                                                                                                                    DB 4,
. 4.82e-01;
                                                                                                                                                                                                                                                                                                  ##cross-references GDB:278285; OMIM:135820
#map_position 22q13.3-22q13.3
KEYWORDS alternative splicing
#Hength 601 #molecular-weight 65485
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##cross-references GDB:27825; OMIM:135820
#map position 22q13.3-22q13.3
KEYWORDS
Alternative splicing; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 96;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 VPLPLLLGGLALLAAGVDADVLLEACC 37
                                                                                                                                                                                                                            ##residues 1-601 ##label ARG
##cross-references GB:X53742
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                                                                                                                                                                                                                                                                                                                                                                                                 h 10.1%;
Similarity 57.1%;
16; Conservative
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F-95, X, 97-107, X', 109-191, X', 193-260, X', 262-278, X', 280-572, X', 574-611, X', 613-656, X', 658-737, X', 739-64, X', 766-809, X', 811-926, X', 928-935, X', 937-1027 ##label MAN we have shown the unidentified residues as Lys forming glycosylated 5-hydroxylysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-95,'X',97-107,'X',109-191,'X',193-260,'X',262-278,'X',286-272,'X',54-611,'X',613-656,'X',658-737,'X',733-764,'X',766-809,'X',811-926,'X',928-935,'X',937-1027 ##label MAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                903-proline modified to 4-hydroxyproline was also found
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cell binding; coiled coil; extracellular matrix;
glycoprotein; homotrimer; hydroxylysine; hydroxyproline;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecular characterization of cuticle and interstitial collagens from worms collected at deep sea hydrothermal
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                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                     #formal_name Riftia pachyptila
22-Nov-1993 #sequence_revision 09-Mar-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S22915
Mann, K.; Gaill, F.; Timpl, R.
submitted to the Protein Sequence Database, July 1992
Amino acid sequence and cell adhesion activity of a
fibril-forming collagen from the tube worm Rifia
pachyptila living at deep sea hydrothermal vents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaill, F.; Wiedemann, H.; Mann, K.; Kuehn, K.; Timpl,
Engel, J.
#length 683 #molecular-weight 74475 #checksum 7443
                                                                                                                                                                                                                                                                                                            S28774 #type fragment collagen alpha chain - tube worm (Riftia pachyptila)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mann, K.; Gaill, F.; Timpl, R.
Bur. J. Blochem. (1992) 210:839-847
Amino-acid sequence and cell-adhesion activity of a
fibril-forming collagen from the tube worm Riftia
pachyptila living at deep sea hydrothermal vents.
$228774
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                                                 Length 683;
                                                                           4.82e-01;
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                                                                                                     3; Mismatches
                                                    Score 96;
Pred. No. 4
                                                                                                                                                                                    10 VPLPLLLGGLALLAAGVDADVLLEACC 37
                                                                                                                                                                                                                                                                                                                                                                                                                                       23-May-1997
S28774; S22915; S17581
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#accession S17581
                                                    Query Match
Best Local Similarity 57.1%;
Matches 16; Conservative
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##residues 1-95,'X'
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##residues 1-95,'X'
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Local Similarity
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KEYWORDS
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##molecule_type protein
##rosidues 136-253 ##label RE4
##rosidues 176-Glx may also be present
##note
NT The first component of complement is a calcium-dependent complex of
the three subcomponents Clq, Clr, and Cls. Subcomponent Clq binds
to immunoglobulin complexes, with resulting serial activation of
Clr (enzyme), Cls (proenzyme), and the other eight components of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Cig subcomponent is composed of nine subunits, six of which are disulfide-linked dimers of the A (see ClHUQA) and B chains, and three of which are disulfide-linked dimers of the C (see ClHUQC) chain. Equimolar amounts of the A, B, and C chains are found after reduction of the disulfide bonds.
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#product complement subcomponent Clq chain B #status
experimental #label MAT\
#domain collagenous, triple helix #label COL\
#domain complement Clq carboxyl-terminal homology #label
                                                                                                                                                                                                                                                                                                                                                                                                       residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement pathway; glycoprotein; heterodimer; hydroxylysine; hydroxyproline; plasma; pyroglutamic acid; triple helix
                                                                                                                                      Reid, K.B.M.
Blochen. J. (1979) 179:367-371
Complete amino acid sequences of the three collagen-like
regions present in subcomponent Clq of the first component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reid, K.B.M.; Gagnon, J.; Frampton, J.
Biochem. J. (1982) 203:559-569
Completion of the amino acid sequences of the A and B chains
of subcomponent Clq of the first component of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #map_position 1p36.3-1p34.1
CLASSIFICATION #superfamily complement subcomponent Clq chain A; complement
Clq carboxyl-terminal homology
Clq carboxyl-terminal homology
                                                                           as
                                                                                                                                                                                                                                                                                                                                                          Reid, K.B.M.; Thompson, E.O.P.
Blochem. J. (1978) 173:863-868
Amino acid sequence of the N-terminal 108 amino acid residue
of the B chain of subcomponent Clq of the first component
of human complement.
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#modified_site pyrrolidone carboxylic acid (Gln) (in
mature form) #status experimental\
#disulfide_bonds interchain (to chain A-26) #status
##molecule_type mRNA
##residues 28-253 ##label RE1
##cross-references EMBL:X03084
##note the authors translated the codon ACA for residue 46
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#blnding_site carbohydrate (Lys) (covalent) #status
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                                                                                                                                                                                                                                                                                                                     RE5
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#accession A90301
##molecule_type_tortein
##residues
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#accession B90315
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##molecule___ypp mRNA
##residues 1-389, G, 391-440 ##label TAR
##cross-references EMBL:X54096; NID:956563; PID:956564
WT The active enzyme catalyzes the transfer of acyl groups from
lecithin to sterol to form sterol esters. Palmitoyl, oleoyl, and
linoleoyl residues can be transferred; a number of sterols,
including cholesterol, can act as acceptor. Apolipoprotein A-I is
a potent activator for this enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Meroni, G.; Malgaretti, N.; Magnaghi, P.; Taramelli, R.
Nucleic Acids Res. (1990) 18:5308
Nucleotide sequence of the cDNA for lecithin-cholesterol acyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *superfamily phosphatidylcholine--sterol acyltransferase acyltransferase; glycoprotein; lipid metabolism; lipoprotein
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phosphatidylcholine--sterol O-acyltransferase (EC 2.3.1.43)
                                                                                                                                                                                                                                                                                                                                                                        XXXTN #type complete phosphatidylcholine--sterol O-acyltransferase (EC 2.3.1.43)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *product phosphatidylcholine--sterol acyltransferase *status predicted *label MAT\ *binding_site carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                             precursor - rat
lectthin-cholesterol acyltransferase precursor;
phospholipid--cholesterol acyltransferase precursor
#formal_name Rattus norvegicus #common_name Norway rat
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preductor - human lecithin--cholesterol acyltransferase precursor; phospholipid--cholesterol acyltransferase precursor #formal_name Homo sapiens #common_name man 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change
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experimental
#length 253 #molecular-weight 26722 #checksum 7399
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submitted to the EMBL Data Library, July 1990
S11302
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                                                                                  Length 253;
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                                                                                                               . 1.96e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transferase (LCAT) from the rat. #cross-references MUID:90384859
                                                                            Score 91; DB 1;
Pred. No. 1.96e+0
                                                                                                                                               6; Mismatches
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                                                                                  9.5%;
Similarity 53.3%;
8; Conservative
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Best Local Similarity 62.5%;
Matches 15; Conservative
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S11214; S11302
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7 KVPWAAVTLLLLLLL
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##residues 1-44(
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RESULT

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A23532
Rao, C.D.; Igarashi, H.; Chiu, I.M.; Robbins, K.C.; Aaronson,
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#journal Science (1983) 220:963-965
#title Human platelet-derived growth factor (PDGF): amino-terminal amino acid sequence.
#cross-references MUID:83197379
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                                                                                                                                                                                                                #journal Science (1984) 225:636-639
#title Transforming potential of human c-sis nucleotide sequences #cross-references MUD:84250225
#accession A94276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chiu, I.M.; Reddy, E.P.; Givol, D.; Robbins, K.C.; Tronick, S.R.; Aaronson, S.A. (2011 (1984) 37:123-129 Nucleotide sequence analysis identifies the human c-sis proto-oncogene as a structural gene for platelet-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:2392-2396
#title Structure and sequence of the human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) transcriptional unit.
#cross-references MUID:86205961
#accession A23532
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FEBS Lett. (1986) 198:344-348
The human osteosarcoma cell line U-2 OS expresses a 3.8
kilobase mRNA which codes for the sequence of the PDGF-B
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Cultured human endothelial cells express platelet-derived
growth factor B chain: cDNA cloning and structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collins, T.; Ginsburg, D.; Boss, J.M.; Orkin, S.H.; Pober,
#formal_name Homo sapiens #common_name man
18-Apr-1984 #sequence_revision 20-Sep-1984 #text_change
20-Mar-1998
A94276; A21024; A23532; A93366; A25141; A94271; A93308;
A443499; S56115; IS7635; I37266; A01380; A94622
A94276
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##residues_1-241 ##label RAO
##cross-references GB:M12783; GB:M16288; NID:g338210; PID:g338211
SNCE A93366 ------ N BORG I.M.: Orkin, S.H.; PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##residues 1-241 ##label JOS
##cross-references GB:K01401; NID:g338206; PID:g338209
:NCE A21024
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##residues 1-241 ##label COL
##cross-references GB:X02811; NID:935371; PID:935372
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##residues 26-241 ##label WEI
##cross-references GB:X03702; NID:g35374; PID:g35375
SNCE A94271
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#cross-references MUD:84205633
#accession A21024
##moloc...
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#cross-references MUID:85296313
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#accession A25141
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Deuel, T.F.; Huang, J.S.; Seeburg, P.H.; Gray, A.; Ullrich,
A.; Scrace, G.; Stroobant, P.; Waterfield, M.D.
EMBO J. (1984) 3:921-928
The c-sis gene encodes a precursor of the B chain of
platelet-derived growth factor.
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hypothetical protein 2 - human
#formal_name Homo sapiens #common_name man
12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change
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18-Nov-1994 #sequence_revision 18-Nov-1994 #text_change
03-May-1996
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Nucleic Acids Res. (1995) 23:2815-2822
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Y #cross-references EMBL:X83705
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platelet-derived growth factor chain B precursor
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11; Mismatches 6; Indels
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Pred. No. 3.38e+00;
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                                                                            29 LQRLLHGDPGEEDGAELDLNMTRSHSGGELESLA-RGRR 66
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                                    1 MSRRSLSLQFPLLLLLLLLPPPPVLLTDAGVPSPVIP-CC
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:18:22 1998; MasPar time 4.81 Seconds 158.235 Million cell updates/sec ü

>US-08-938-548A-6 (1-130) from USO8938548A.pep 954 1 MNLPSTKVPWAAVTLILLL......GRRCPTATATALAPRGGSRV 130 ular output not generated.

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

63816 seqs, 5850866 residues

Searched:

Database:

a-issued 1:5\_COMB 2:PCT9\_COMB 3:backfiles

Mean 27.785; Variance 127.171; scale 0.218 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		æ					
Result No.	Score	Query Match	Query Match Length	DB	a	Description	Pred. No.
				1			•
)	92	9.6	220	m	5175255-4	Patent No. 5175255.	4.65e+00
7	89	9.3	241	m	5194596-15	Patent No. 5194596.	7.65e+00
m	89	9.3	241	H	US-08-387-	Sequence 4, Applicatio	7.65e+00
4	89	9.3	241	~	PCT-US96-0	Sequence 9, Applicatio	7.65e+00
'n	88	9.5	254	~	US-08-236-	4	ď
9	87	9.1	226	m	5498600-2	Patent No. 5498600.	
7	87	9.1	241	٣	5175255-2	Patent No. 5175255.	1.06e+01
80	87	9.1	241	m	5175255-8		1.06e+01
6	87	9.1	282	Н	US-08-445-	Sequence 1, Applicatio	1.06e+01
10	85	8.9	241	ч	US-08-469-	13,	1.47e+01
11	82	8.9	613	~	PCT-US94-1	7	Н
12	84	8.8	238	-	US-08-240-	7	1.73e+01
13	84	8.8	238	Н	US-08-453-	7	1.73e+01
14	84	8.8	1239	Н	US-08-026-	'n	1.73e+01
15	83	8.7	235	7	PCT-US94-0	o,	~
16	83	8.7	235	Н	US-08-243-	ø	2.04e+01
17	82	8	241	٣	5219739-15	.5	2.39e+01
18	80	8.4	492	ч	US-07-794-	Sequence 4, Applicatio	3.29e+01
19	80	8.4	492	Н	US-08-001-	4	3.29e+01
20	80	8.4	1337	7	PCT-0S95-0	'n	3.29e+01
21	79	8.3	589	~	PCT-US91-0	~	
22	79	æ .3	589	Н	us-01-668-	7	3.86e+01
23	78	8.5	1184	٦	US-08-446-	20,	4.52e+01

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Sequence 20, Application Sequence 13, Application Sequence 8, Application Sequence 5, Application Sequence 5, Application Sequence 10, Application Sequence 10, Application Sequence 36, Application Sequence 37, Application Sequence 7, Application Sequence 7, Application Sequence 6, Application Sequence 2, Application Sequence 13, Appl		AA.			lson, Margery IFICATION OF PLATELET-	DB 3; Length 220; 65e+00; .ches 6; Indels 5;	-RGRR 60      CPGRR 113	AA.		JUDITH A.; FIDDES, ULAR ENDOTHELIAL CE
US - 08 - 446 - US - 08 - 097 - US - 08 - 097 - US - 57 - US - 08 - 087 - US - 08 - 08 - 08 - US - 08 - 08 - 08 - US - 08 - 08 - US - US - 08 - 08 - US - U	ALIGNMENTS	PRT; 238			Arlen R.; Nicholson, M METHODS FOR PURIFICATI : 9 DATA: R: US/06/25,344 AR-1987 NW; 307752 CN;	Score 92; Pred. No. 4 10; Mismat	GGELESLA  :   : GAELEPYP	PRT; 261		MUND G.; ABRA ODUCTION OF 2 TA: US/07/450, 8
8.2 1184 1 8.2 1187 1 8.2 1187 1 8.1 1887 1 8.1 831 1 8.1 831 1 8.1 2509 1 8.0 231 1 8.0 231 2 8.0 231 2 8.0 231 2 8.0 231 2 8.0 231 2 8.0 231 2 8.0 488 1 8.0 488 1 8.0 488 1 8.0 488 1 8.0 484 1 7.9 447 1		STANDARD;		75255	75255 INTERPOSEDIO INTERPOSEDIO H FACTOR PEDICATION TION NUMBER DATE: 23-MI	# 5	OPGEEAGAELDLNWTRSHS :  :         :: N-GNHA-AGI-LTMGR-RA	STANDARD;	194596.	4596 TISCHER, RICHARD L. INVENTION: SEQUENCES PPLICATION NUMBE
225 226 226 227 228 233 233 333 333 333 333 334 337 337 338 338 338 338 338 338 338 338		5175255-4	XXXXXX		Then it is in it is i	Match Local Simil es 18;	23 LORLLHGDPGEEA       :::  :  79 LORLLQAN-GNHA	SULT 2 5194596-15 XXXXXX 01-JAN-1900	Patent No. 51	Patent No. 519 APPLICANT: C.;MITCHELL, R TITLE OF I GROWTH FACTOR UNMBER OF CURRENT AP
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APPLICANT: Thomason, Arlen R.;Nicholson, Margery
TITLE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
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TITLE OF INVENTION: METHODS FOR PURIFICATION OF
DERIVED GROWTH FACTOR
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Pred. No. 1.06e+01;
11; Mismatches 6;
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Pred. No. 1.06e+0
11; Mismatches
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APPLICATION NUMBER: US/06/25,344
FILING DATE: 23-MAR-1987
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/25,344
FILING DATE: 23-MAR-1987
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SEQUENCE 261 AA; 29370 MW; 369384 CN;
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Local Similarity 43.6%;
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Local Similarity 43.6%;
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                                                                                               STANDARD;
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TITLE OF INVENTION: BIOLOGICALLY ACTIVE MOSAIC PROTEINS
NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,776
FILING DATE: 07-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 926,149
FILING DATE: 05-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 87; DB 3; Length 226;
Pred. No. 1.06e+01;
11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                 OPERATING SYSTEM: Apple 7.5.3
SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,918A
FILING DATE: 06-May-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 88; DB 1; L
Pred. No. 9.02e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 LQRLLQGDSGKEDGAELDLNMTRSHSGGELESLA-RGKR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2801-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
FENCE 254 AA; 26624 MW; 316872 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 226
SEQUENCE 245 AA; 27563 MW; 324570 CN;
COMPUTER: Apple Power Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 379,239
FILING DATE: 11-JUL-1989
APPLICATION NUMBER: 941,970
FILING DATE: 15-DEC-1986
APPLICATION NUMBER: 896,485
FILING DATE: 3-AUG-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 705,175 FILING DATE: 25-FEB-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 660,496 FILING DATE: 12-OCT-1984
                                                                                                                                                                                                                                                                                              TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                           : 254 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 43.6%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.2%;
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 VPWAAVT-LLLLLLPPA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 LPWALVAGLLLLLLLAAA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5498600
                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1900
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ID 5498600-2
XX
AC XXXXXX
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DT 01-JAN-1900
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XX
CC Patent No.
CC Patent No.
CC APPLICA
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Length 241;

SEQUENCE

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Length 241;

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Sequence 2, Application US/08453943
Patent No. 5738844
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 238;
                        Score 84; DB 1; Length 238;
Pred. No. 1.73e+01;
                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version 5.1a
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Pred. No. 1.73e+01;
2; Mismatches 3;
                                                                                                                                                                                                                                                                   238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUFTWARE: MICTOSOFT WORD for Apple, Ve.
CURRENT APPLICATION DATA:
APPLICATION NATA:
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION:
                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/240,124
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 238 AA, 26350 MW; 315668 CN;
                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 281
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: SATUE STATE STATE STATE: WASHINGTON COUNTRY: USA ZIP: 98101 COMPUTER READABLE FORM: WEDIUM TYPE: Floppy disk COMPUTER: Apple Macinton OPERATING SYSTEM: Apple System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 756822
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 238 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (206) 587-04
(206) 233-0644
                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                              11 AAVILLILILIPP-ALLSI 28
                                                                                                                      2 AAAPLLLLLLLVPVPLLPL 20
                        Query Match 8.8%;
Best Local Similarity 68.4%;
Matches 13; Conservative
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Best Local Similarity 68.4%;
Matches 13; Conservative
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Patent No. 5516658
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CENERTIL DUGGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
                                                                                                                                                                                                                     ö
                                                                                                                                                                  Score 85; DB 2; Length 613;
Pred. No. 1.47e+01;
13; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: STADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
COMPATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,124
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FILING DATE: 30-AUG-1993
APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
                                                                   TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
SEQUENCE 613 AA; 67034 MM; 1960405 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
FENCE 238 AA; 26350 MW; 315668 CN;
                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08240124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
LENGTH: 613 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                  Query Match 8.9%;
Best Local Similarity 31.1%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
                          TYPE: AMINO STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
ID US-08-240-124-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
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SQ SEQUENCE 235 AA; 26415 MW; 293990 CN;

Score 83; DB 2; Length 235; Pred. No. 2.04e+01; 6; Mismatches 1; Indels Query Match
Best Local Similarity 55.6%;
Matches 10; Conservative

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Search completed: Thu Jul 30 09:18:32 1998 Job time : 10 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:12:27 1998; MasPar time 5.42 Seconds 217.356 Million cell updates/sec llar output not generated. . . .

>US-08-938-548A-4 (1-28) from US08938548A.pep 196 1 RSGPPGLQGRLQRLLQASGNHAAGILIM 28 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

Post-processing:

Searched:

140542 seqs, 42109429 residues

Minimum Match 0% Listing first 45 summaries

Database:

sptrembl5
1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_hub 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Mean 29.922; Variance 51.029; scale 0.586 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	-	
wesult No.	Score	Query Match	o Query Match Length DB	DB	a	Description	Pred. No.
-	76	38.8	1174	. 4	095168	TIGHT JUNCTION PROTEIN	1.91e-01
7	70	35.7	249	10	P97382	K+ CHANNEL BETA4 SUBUN	1.73e+00
m	70	35.7	1277	10	035821	PAR INTERACTING PROTEI	1.73e+00
4	69	35.2	439	σ	052495	HRPE.	2.48e+00
·w	69	35.2	568	ო	027212	ARTICULIN P60.	2.48e+00
9	69	35.2	1465	m	017909	н06001.2.	2.48e+00
7	99	34.7	178	σ	031955	YONC PROTEIN.	3.53e+00
œ	68	34.7	580	10	060811	RETINOID X RECEPTOR IN	3.53e+00
თ	67	34.2	462	9	P95644	RNA POLYMERASE SIGMA F	5.01e+00
10	67	34.2	210	σ	059913	RNA POLYMERASE SIGMA F	5.01e+00
11	49	34.2	514	σ	P77951	RNA POLYMERASE SIGMA F	5.01e+00
12	67	34.2	525	σ	059813	RNA POLYMERASE SIGMA F	5.01e+00
13	67	34.2	528	g	059814	RNA POLYMERASE SIGMA F	5.01e+00
14	67	34.2	972	H	P89521	POLYPROTEIN.	5.01e+00
. 15	67	34.2	1841	σ	033958	TYLACTONE SYNTHASE MOD	5.01e+00
16	29	34.2	2115	7	014980	NUMA PROTEIN.	5.01e+00
17	67	34.2	2591	σ	054959	PRISTINAMYCIN I SYNTHA	5.01e+00
18	99	33.7	331	12	091640	LEUCINE ZIPPER WITH BA	7.09e+00
19	99	33.7	633	6	007309	NODO.	7.09e+00
20	99	33.7	1344	10	035851	P160 MYB-BINDING PROTE	7.09e+00

1.00e+01	1.00e+01	1.00e+01	1.00e+01	1.41e+01	1.41e+01	1.41e+01	1.41e+01	1.41e+01	1.41e+01	1.97e+01	1.97e+01	1.97e+01	1.97e+01	1.97e+01	1.97e+01	1.97e+01	2.75e+01	2.75e+01	2.75e+01	2.75e+01	2.75e+01	2.75e+01	2.75e+01	2.75e+01
MOUSE 57-KD CALCIUM-BI	HYPOTHETICAL 33.8 KD P	3-HYDROXYISOBUTYRYL-CO	F14D7.2.	ORF263.	METHYLTRANSFERASE.	CARA.	PROTEIN-TYROSINE PHOSP	FROM BASES 1860594 TO	HSGAK.	PUTATIVE SIGMA-54 DEPE	HYPOTHETICAL 37.6 KD P	THYROID HORMONE INDUCE	ORF351.	HYPOTHETICAL 41.3 KD P	POLYPROTEIN.	POLYPROTEIN.	HYPOTHETICAL 10.2 KD P	DEOXYCYTIDINE-TRIPHOSP	RNA-DIRECTED DNA POLYM	CONSERVED PROTEIN.	RETINA SPECIFIC RGS PR	UNC-104 - AND KIFIA-REL	RNA POLYMERASE SIGMA F	PRISTINAMYCIN I SYNTHA
062041	033744	092931	019452	031722	032855	050983	027932	P76237	014976	050872	P74570	091654	038320	969600	082731	082720	054084	027642	005804	026847	P79348	013355	059532	007944
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178	312	381	457	263	310	377	548	256	1311	140	331	335	351	365	972	972	101	150	319	345	374	476	574	4848
33.2	33.2	33.2	33.2	32.7	32.7	32.7	32.7	32.7	32.7	32.1	32.1	32.1	32.1	32.1	32.1	32.1	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6
65	65	65	65	64	64	64	64	64	64	63	63	63	63	63	63	63	62	62	62	62	62	62	62	62
21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	. 38	39	40	41	42	43	44	45

## ALIGNMENTS

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	PRT; 1174 AA.		CREATED).	LAST SEQUENCE UPDATE)	LAST ANNOTATION UPDATE)				VERTEBRATA; TETRAPODA; MAMMALIA;					•					BEATCH M., JESAITIS L.A., GALLIN W., GOODENOUGH D.A.,		5(1996).				SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.				SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.		V; 2FA16B83 CRC32;	Score 76; DB 4; Length 1174;	atches 8: Indels	
	PRELIMINARY;		(TREMBLREL. 02,	(TREMBLREL. 02,	(TREMBLREL. 05,	TIGHT JUNCTION PROTEIN.		CANIS FAMILIARIS (DOG).	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;	ARNIVORA.		FROM N.A.	94179414.	A., GOODENOUGH D.A.;	J. CELL BIOL. 124:949-961(1994)		OM N.A.	96421547.	JESAITIS L.A., GALI	.к.;	. BIOL. CHEM. 271:25723-25726(1996)		OM N.A.	D.A.;	MAR-1994) TO EMBL/G	·	OM N.A.		AUG-1996) TO EMBL/G	EMBL; L27152; G1536970;	1174 AA; 132085 MW;	38.8%; Sc Gimilarity 35.7%; Dy	rvative,	)
RESULT 1	095168	_			01-JAN-1998			-			[1]	SEQUENCE	MEDLINE;		_		SEQUENCE	MEDLINE;	_		ט	[3]		_				•				Query Match		
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249 AA. PRT; PRELIMINARY;

RESULT 2 ID P97382

TO EMBL/GENBANK/DDBJ DATA BANKS

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SEQUENCE
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                                                                                                               Query Match
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P95644;
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AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
BORRISS R., BOURSIER L., BRANS A., BRAUN M., BRIGHELL S.C., BRON S.,
RA BROULLET S., BRUSCHI C.V., CALDMELL B., C., EMERSON P.T.,
RA BULLIST S., BRUSCHI C.V., CALDMELL B., CAPTER N.J.,
CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
BENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D., FERITZ C.,
GLASER P., GOPFEAU A., GOLIGHTIX E.J., GRANDI G., GUISEPPI G., GUY B.J.,
HAGGA K., HAIECH J., HARWOOD C.R., HENAUT A., HILBERT H., HOLSAPPEL S.,
RASHARA Y., KLAERR-BLANCHARD M., KLEIN C., KOBAYASHI Y., KOETTER P.,
KONINGSTEIN G., KROGH S., KUMANO M., KURITA K., LEVINE A., LIU H.,
ANDINOIS S., LAUBER J., LAZARRUL V., LEE S.M., LEVINE A., LIU H.,
ANDINOIS S., MAUEL C., MEDIGUE C., MEDINA N., MELLADO R.P., MIZUNO M.,
ANDEL C., NAKAI S., NOBAGK M., NOONE D., O'RELLIY M., CORMA K.,
COLWARA A., OUDEGA B., PARK S.H., PARKO V., POHI T.M., PORTETELLE D.,
ANDINOIS S., MANDEL C., SEKIGUCHI J., SEKOWSKA A., SEROR S.J.,
ANDORT G., REY M., SEXNOLDES S., RIEGER M., SHOLLE C., PURRELLE B.,
A RADOPORT G., REY M., SADALE Y., SEKIGUCHI J., SEKOWSKA A., SEROR S.J.,
A SCHROETER R., SCOFFONE F., SEKIGUCHI J., SEKOWSKA A., TARAGI T.,
TARAHASHI H., TARKEMARU K., TARECHI M., TAMANGSHI R., WEDLER E.,
ANDINER F., VASSAROTI A., VIARI A., WABBUTT R., WEDLER E., WEDLER E.,
ANDINER F., VASSAROTI A., VIARI A., VANDENBOL M.,
ANDINER F., VASSAROTI A., VIARI A., YAMMOTO H., YAMANE K.,
ANDINER F., VASSAROTI A., VIARI A., YAMANOTO H., YAMANE K.,
ANDINER F., VASSAROTI A., VIARI A., YAMANOTO H., YAMANE K.,
ANDINER F., VALLER E., YALRI A., YANDENER E.,
ANDINER F., VASSAROTI A., VIARI A., YAMANOTO H., YAMANE K.,
ANDINER F., VALLE R., YANDENER F., YORLER E.,
ANDINER F., VALLE R., YORLE A., YAMANOTO H., YAMANE K.,
ANDINER F., VALLE A., YAMANOTO H., YAMANE K.,
ANDINER F., VALLE A., YANDEN E., YANDELER E., WELLE E., WILLE E., WILLE E., YANDENDER E.,
ANDINER F., VASSAROTIN A., YANDEN E., YANDENER E.,
ANDINER 
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                                                             MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPERY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MAUNTRAN A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
MATSON A., WEINSTOK L., WILKINSON-SPROAT J., WOHLDMAN P.;
NATURE 368:32-38(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACILLUS SUBTILIS.
PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z92970; E349623; -.
PROSITE; PS00598; CHROMO_1; 2.
SEQUENCE 1465 AA; 169391 MW; F959D52F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 69; DB 3; Lv
Pred. No. 2.48e+00;
3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TREMBLREL. 05, 01-JAN-1998 (TREMBLREL. 05, 01-JAN-1998 (TREMBLREL. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 35.2%;
Local Similarity 69.2%;
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NATURE 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TREMBLREL. 01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  700 QGRLQQLLKSSGK 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 QGRLQRLLQASGN 20
                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           031955
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BARRIL A., CONCHA M.I., FIGUEROA J., LEON G.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y10835; E294130; -
PROSITE; PS00715; SIGMA70_1; 1.
PROSITE; PS00716; SIGMA70_2; 1.
TRANSCRIPTION REGULATION; SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE; DNA-BINDING.
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 67; DB 9; Length 462;
Pred. No. 5.01e+00;
11; Mismatches 4; Indels
                                                            Indels
                                                                                                                                                                                                                                                    EUBACTERIA; FIRMICUTES; ACTINOMYCETES; RENIBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAY-1997 (TREMBLREL. 03, CREATED)
01-WAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 68; DB 10; Leg
Pred. No. 3.53e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               462 AA; 50504 MW; E54BBFE5 CRC32;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL; 299115; E1183561; -.
SEQUENCE 178 AA; 19609 WW; CA7B8EDO CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            580 AA; 64852 MW; 28DA7406 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               462 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 95280959.
SEOL W., CHOI B.S., MOORE D.D.;
MOL. ENDOCRINOL. 9:72-85(1995).
EMBL; UZ2015; G709961; -
MGD; MGI:103185; RXRIP110.
                                                                                                                                                        20
                                                                                                                                                                                            7 LOGRIORLIQASGNHAAGIL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.2%;
llarity 31.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              485 QGRLLSLLEQSEHRTTGV 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA POLYMERASE SIGMA FACTOR
                                                                            Match 34.7%;
Local Similarity 45.0%;
es 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 44.4%;
les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||| ||: | :::|:
QGRLQRLLQASGNHAAGI 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RENIBACTERIUM SALMONINARUM
                                                                                                                                                        1 MATRLQKALTEVGNHTTGNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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STREPTOMYCES FRADIAE.
PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.
                                                                                                                                                                                                                                                                                                                                          Score 67; DB 11; Length 972;
Pred. No. 5.01e+00;
10; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 67; DB 9; Length 1841;
Pred. No. 5.01e+00;
9; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEHOFF B.S., SUTTON K.L., ROSTECK P.R. JR.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U78289; G2317864; -.
PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
                                                                                                                                                                                                      STRAIN-Y-6;
SUZUKI S., KIMURA M., KUSUDA R.;
SUBHITED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AB001329; D1019990; -
EMBL; AB006783; D1022914; -.
                                                                                                                                      SUZUKI S., KIMURA M., KUSUDA R.;
SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
101-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
POLYPROTEIN
BIRNAVIROS SP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAST SEÓUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                   VIRUSES; DSRNA VIRUSES; BIRNAVIRIDAE; BIRNAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1841 AA; 191190 MW; 2FF1A058 CRC32;
                                                                                                                                                                                                                                                                                                           972 AA; 106767 MW; 9905CA0D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1841 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQ
01-JAN-1998 (TREMBLREL. 05, LAST ANN
TYLACTONE SYNTHASE MODULE 7.
                                                                                                                                                                                                                                                                                                                                                                                                            731 RTTASGMDEELQKLLHATMARAKEV 755
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RSGPPGLQGRLQRLLQASGNHAAGI 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                        74.2%;
Local Similarity 32.0%;
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jery Match 34.2%;
sst Local Similarity 33.3%;
stches 8; Conservative
                                                                                                    SEQUENCE FROM N.A. STRAIN-Y-6;
                                                                                                                                                                                     SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                             SEQUENCE
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033958
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                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
ID 03
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Search completed: Thu Jul 30 09:12:50 1998 Job time: 23 secs. ò

1513 RDTPAALAAHLAELLATARDHGPG 1536

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Matches

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Gaps

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:14:41 1998; MasPar time 5.30 Seconds 376.024 Million cell updates/sec : 0

bular output not generated.

>US-08-938-548A-6 (1-130) from US08938548A.pep 954 1 MNLPSTKVPWAAVTLLLLLL......GRRCPTATALAPRGGSRV 130 Title: Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

124785 seqs, 15338987 residues

Searched:

Minimum Match 0% Listing first 45 summarles Post-processing:

a-geneseg31-2
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 Database:

Mean 29.913; Variance 129.900; scale 0.230 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Result No.	Score	Query Match	ouery Match Length DB	DB	GI.	Description	Pred. No.
-	96	10.1	566	7	R11148	Fibulin A.	5.91e+00
7	96	10.1	601	~	R11149	Fibulin B.	5.91e+00
m	96	10.1	683	N	R11150	Fibulin C.	5.91e+00
4	91	9.5	440	~	P70134	Natural recombinant h	1.39e+01
S	91	9.5	440	25	W24789	Human lecithin-choles	1.39e+01
9	83	9.3	190	σ	R50012	Truncated Platelet de	1.94e+01
7	8	9.3	216	12	R68617	Human PDGF-B precurso	1.94e+01
8	83	9.3	220	<b>c</b>	R40965	rPDGF B.	1.94e+01
o,	8	9.3	241	σ	R50009	Platelet-derived Grow	1.94e + 01
10	8	9.3	241	12	R63469	Recombinant platelet	1.94e + 01
11	83	9.3	241	σ	R50002	Platelet-derived Grow	1.94e+01
12	83	9.3	241	ω	R40964	PDGF Bc-sis.	1.94e+01
13	8	9.3	241	Н	P80596	Recombinant platelet	1.94e + 01
14	88	9.5	252	4	R21708	HSV-1 (CVG-2) ICP34.5	2.30e+01
15	88	9.5	254	12	R64190	Human 4-1BB-L polypep	2.30e+01
16	88	9.5	254	25	W26657	Human 4-1BB ligand.	2.30e+01
17	87	9.1	111	7	R35515	Tryptophan aporepress	2.72e+01
18	87	9.1	190	12	R60615	Human PDGF-B 109 subu	2.72e+01
19	87	9.1	201	4	R21443	Sequence encoded by p	2.72e+01

2.72e+01 2.72e+01 2.72e+01 2.72e+01 2.72e+01 2.72e+01 2.72e+01 2.72e+01 3.72e+01 3.79e+01 3.79e+01 3.79e+01 4.47e+01 4.47e+01 5.26e+01 5.26e+01 6.20e+01 7.29e+01 8.58e+01
V-sis protein p288is. CV-sis gene encoded P Recombinant platelet CV-sis gene product. Recombinant platelet PLOGE BV-sis. Human PDGF-B 119 link Prostaglandin endoper Recombinant platelet Sequence encoded by t Porrine complement in Human endothelin-bomb Truncated E protein f Eph transmembrane tyr Human hek-L protein. Glutamic acid recepto Human S86/S109 FLE3 Human flt-3 ligand. S. clavuligerus ORF1 Amino acid sequence o Human Platelet Derive Wild-type avidin prot Wzy (Rfc) protein inv
R22673 P80597 R469472 R4609677 R63468 R63468 R61029 P81029 P81029 P81029 P81029 P81029 P81029 P81029 P81029 R61481 R61945
112 113 113 113 113 113 113 113 114 117 117 117 117 117 117 117 117 117
226 2411 2411 2411 2711 2711 2711 2711 2711
$\begin{array}{c} \mathbf{u} \circ $
8877788882747884747874747874747474747474
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## ALIGNMENTS

RESULT

d. Brotein. 566 aa	בוחרביווי, החח	first entry)		n; adhesion; receptor; fibronectin.		Location/Qualifiers		/label= signal sequence	;	/label- fibulin A	,	/label- N-linked glycosylation	24 . 1 . m. 1. m. 2	/label= N-linked glycosylation	/label- N-linked glycosylation		/label= type I motif		/label- repeat unit l		/label _ repeat unit 2		/label Glu/Asp-rich region	1	/label type II motit		/label = repeat unit l		/label= consensus pentapeptide	/label= repeat unit 2	1	/label= consensus pentapeptide		/label= repeat unit 3		/label= consensus pentapeptide			
D11118 standard.	R11148;	_	Fibulin A.	Beta-1 integrin;	Homo sapiens.	Key	peptide		protein	,	modified_site		modified_site	modifing 01+0	2212	region	1	region		region	•	region		region		region	•	region	1	redton	region	ì	region		region	40	TedTon	region	101601
TES C	12	Z	DE	ΚW	os	FН	FI	FI	E :	FI	F	Ħ	E		4 E-	댐	ΕŢ	FT	F	Εď	F	FI	E I	EH	FI	FŢ	E I	5	- E	1 4	FI	F	FT	FJ	FI	F.	7 E	- E-	,

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:11:23 1998; MasPar time 4.07 Seconds 251.156 Million cell updates/sec uo um

>US-08-938-548A-4 (1-28) from USO8938548A.pep 196 1 RSGPPGLQGRLOALGASGNHAAGILIM 28 ular output not generated. Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

120441 seqs, 36531193 residues

Searched:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d Database:

Mean 30.060; Variance 54.689; scale 0.550 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Pred. No.	3.92e+00	3.92e+00	5.47e+00	7.60e+00	7.60e+00	7.60e+00	7.60e+00	7.60e+00	7.60e+00	7.60e+00	1.05e+01	1.45e + 01	1.45e+01	2.00e+01	2.00e+01	2.00e+01	2.00e+01	2.00e+01	2.00e+01	2.00e+01	2.00e+01	2.74e+01	2.74e+01
Description	hrpE protein - Pseudo	mALDP protein - mouse	hypothetical protein		transcription initiat	transcription initiat	transcription initiat	transcription initiat	YOR1 protein - yeast	NuMA protein - human	E2 protein - human pa	calcium-binding prote	adenylate cyclase (EC	hypothetical protein	BGRF1 protein - human	ribosomal protein S2,	hypothetical protein	protein-tyrosine-phos	protein-tyrosine-phos	hypothetical protein	hypothetical protein	pulmonary surfactant	pulmonary surfactant
Ω	561858	S47044	E69913	JH0496	S11712	S41307	JN0443	JN0445	S64616	S23647	S36593	S26481	A33988	S51155	QQBE38	A42115	S76929	A46101	B46101	B64939	H64888	LNHUPS	LNHUP1
92	7	7	~	7	7	7	~	7	~	~	N	N	~	N	Н	~	7	7	N	~	7	Н	Н
% Query Match Length DB	439	736	178	442	442	510	525	528	1477	2115	461	178	1692	263	325	394	400	535	548	556	879	248	248
% Ouery Match	35.2	35.2	34.7	34.2	34.2	34.2	34.2	34.2	34.2	34.2	33.7	33.2	33.2	32.7	32.7	32.7	32.7	32.7	32.7	32.7	32.7	32.1	32.1
Score	69	69	. 68	67	29	29	67	29	29	67	99	65	65	64	9	64	64	64	64	. 64	9	63	63
Result		7	m	4	'n	ø	7	ω	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23

847044 #type complete
mALDP protein - mouse
#formal\_name Mus musculus #common\_name house mouse
113-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change
10-Sep-1997
847044
847044

ACCESSIONS REFERENCE

TITLE ORGANISM DATE

2.74e+01 2.74e+01 2.74e+01 2.74e+01	2.74e+01 2.74e+01 2.74e+01 2.74e+01 2.74e+01 3.75e+01	3.75e+01 3.75e+01 3.75e+01 3.75e+01 3.75e+01 3.75e+01	3.75e+01 3.75e+01 3.75e+01 3.75e+01 3.75e+01 3.75e+01
HH!	hypothetical protein hypothetical protein ecdysone receptor - f genome polyprotein - PASI protein - yeast allergen TBA-1 - Toxo	transcription factor hypothetical protein hypothetical protein RNA-directed DNA poly conserved hypothetica carboxypeptidase (EC	sulfite reductase (fe genome polyprotein . nitrite reductase (NA fatty-acid synthase ( fatty-acid synthase ( fatty-acid synthase (
LNHUP6 151921 Q3YCRQ LURT3	S76765 S09852 A41055 GNXSIV A55152 B49139	S48361 S49183 B64899 S19248 F69200 JC2294	RDYCS7 GNXSN1 A49848 A57788 B57788
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248 256 324	331 429 878 972 1157 36	187 253 281 319 345	624 972 1176 2504 2504 2509
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225 24 25 26	3 3 3 5 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	# # # # # # # # # # # # # # # # # # #	9 4 4 4 4 4 9 4 6 6 6 6 6

## ALIGNMENTS

S61858 #type complete hrpE protein - Pseudomonas solanacearum #formal_name Pseudomonas solanacearum		so .	Boucher, C.  Boucher, C.  Mol. Microbiol. (1995) 15:1095-1114  Le The hrp gene locus of Pseudomonas solanacearum, which controls the production of a type III secretion system, encodes eight proteins related to components of the beatoning in the production of the beatoning the process	ssion S6 status molecule_ty residues cross-refer	S S hrpE e hrpE ICATION #superfamily H+-transporting ATP synthase alpha chain homology	#domain H+-transporting ATP synthase alpha chain homology #label ATP #1533 #checksum 9718 #length 439 #molecular-weight 47533 #checksum 9718	Match Local Similarity 44.4%; Pred. No. 3.92e+00; es 12; Conservative 7; Mismatches 8; Indels 0; Gaps 0;	281 RGFPPSVFAELPRLLERAGMSAAGSIT 307  :   ::      : :      :  1 RSGPPGLQGRLQRLLQASGNHAAGILT 27	2
RESULT ENTRY TITLE ORGANISM	DATE	REFERENCE #authors	#journal #title	#accession ##statu ##molec ##resid ##cross	GENETICS #gene CLASSIFICATION	FEATURE 191-359 SUMMARY	Query Match Best Local Matches	Db 281	RESULT

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##molecule_type DNA
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 JN0443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marcos, A.T.; Diez, B.; Gutierrez, S.; Fernandez, F.J.; Velasco, J.; Martin, J.F. submitted to the EMBL Data Library, December 1993 Organization and expression of the hrdB-sprc gene cluster of streptomyces griseus encoding a sigma factor protein and a serine protease. Role on growth and sporulation of
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Gene (1995) 12c:63-70
Four genes in Streptomyces aureofaciens containing a domain characterstic of principal sigma factors.
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                                                                       *superfamily transcription initiation factor sigma katF; transcription initiation factor sigma katF homology
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transcription initiation factor sigma homolog hrdB -
Streptomyces aureofaciens
#formal_name Streptomyces aureofaciens
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #domain transcription initiation factor sigma katr
homology #label KTF
#length 510 #molecular-weight 55795 #checksum 1415
                                                                                                                                            #domain transcription initiation factor sigma kat?
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                                                                                                                                                                                #length 442 #molecular-weight 48413 #checksum 4794
                                                                                                        DNA binding; sigma factor; transcription initiation
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                                                                                                                                                                                                                     Length 442;
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Pred. No. 7.60e+00;
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EMBL: X52983; NID: 948744; PID: 948745
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Pred. No. 7.60e+00;
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                                                                                                                                                                 homology #label KTF
                  ##experimental_source strain A3(2)
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                                                                                                                                                                                                                                                                                            370 LQEQLHSVLDTLSEREAGVVSM 391
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31.8%;
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Similarity 31.8%;
7; Conservative
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Matches 7; Conservative
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Kormanec, J.; Farkasovsky, M.; Poutuckova, L.
Gene (1992) 12:68-70
Four genes in Streptomyces aureofaciens containing a domain
characterstic of principal sigma factors.
                                                                                                                 *superfamily transcription initiation factor sigma katF; transcription initiation factor sigma katF homology DNA binding; sigma factor; transcription initiation
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transcription initiation factor sigma katf homology
DNA binding; sigma factor; transcription initiation
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homology #label KTF
#length 528 #molecular-weight 57598 #checksum 7360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #formal_name Streptomyces aureofaciens
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
08-Sep-1997
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#length 525 #molecular-weight 57204 #checksum 9676
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transcription initiation factor sigma homolog hrdE
Streptomyces aureofaciens
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YOR1 protein - yeast (Saccharomyces cerevisiae)
protein 69537; protein YGR281w
#formal_name Saccharomyces cerevisiae
17-May-1996 #sequence_revision 17-May-1996 #texi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 67; DB 2; Length 520,
Pred. No. 7.60e+00;
"...matches 5; Indels
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Immission submitted to the Protein Sequence Database,
cession S64616
##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues 1-528 ##label KOR
##cross-references GB:M90412; NID:g153308; PID:g153309
##residues 1-525.##label KOR
##cross-references GB:M90411; NID:g153305; PID:g153306
                                                                                                                                                                                                                                                                                                                                                          Score 67; DB 2; L
Pred. No. 7.60e+00;
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Best Local Similarity 36.4%;
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Best Local Similarity 31.8%;
Matches 7; Conservative
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PGLQGRLQRLLQASGNHAAGILT 27
                                            ##residues
                                                                                                                                                                                                                                                                         CLASSIFICATION
SUMMARY
                                                                                                                                                                                                                                                        contents
                                                                                                                                                                    #journal
#title
                                                                                                        #authors
                                                                                   REFERENCE
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                                                                                                                       ##residues 1-1692 ##label YAM
##cross-references GB:M24942; NID:g173378; PID:g173379
##note the authors translated the codon TGC for residue 626 as
Ser, and GCC for residue 1243 as G1y
FICATION #superfamily leucine-rich alpha-2-glycoprotein repeat
homology; yeast adenylate cyclase catalytic domain homology
DS phosphorus-oxygen lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Landgren, M.; Zetterstrand, M.; Sundberg, E.; Glimelius, K. submitted to the EMBL Data Library, January 1995 Mitochondrial analysis revealed transcription of an ORF 3 of the atp6-gene and translation of a 32 kD protein in alloplasmic male sterile Brassica lines containing the B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
#journal Mol. Biol. Med. (1983) 1:21-45
#title Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8
#cross-references MUID:85035713
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yeast: a comparison of the genes from pombe and Saccharomyces cerevisiae.
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BGRF1 protein - human herpesvirus 4 (strain B95-8)
#formal_name human herpesvirus 4, Epstein-Barr virus
25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #formal_name mitochondrion Brassica tournefortii
19.Mar-1997 #sequence_revision 19-Mar-1997 #text_change
10.Sep-1997
S51155
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                                                                                                                                                                                                                                                                                                                  homology #label YACC
#length 1692 #molecular-weight 190332 #checksum 2609
                                                                                                                                                                                                                                                                                              #domain yeast adenylate cyclase catalytic domain
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mitochondrion
#length 263 #molecular-weight 29082 #checksum 9529
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hypothetical protein 263 - Brassica tournefortii
mitochondrion
                                                                                                                                                                                                                                                                                                                                                                              Length 1692;
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##cross-references EMBL:X83692; NID:g633155; PID:g633157
                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 64; DB 2; Length 263;
Pred. No. 2.00e+01;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                              Score 65; DB 2; Lv
Pred. No. 1.45e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tournefortii cytoplasm
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A43044; A03782; S33034
#title Adenylate cyclases in
Schizosaccharomyces
#cross-references MUID:89345533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : |||:|| |: ||:|
7 LQGRLQRLLQASGNHAAGIL 26
                                                                                 preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKNRLQWLLPLLGSSVAGFL 20
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llarity 57.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 32.7%;
Best Local Similarity 45.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1539 PVQLQGRLERLIKS 1552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 PPGLQGRLQRLLQA 17
                                                                                                        ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                              A33539
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REFERENCE
#authors
#submission
#description
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                                                                                   ##status
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#authors
#journal
#title
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WORDS
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Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.;
Farrell, P.J.; Gibson, T.J.; Hatfull, G.; Hudson, G.S.;
Satchwell, S.C.; Seguin, C.; Tuffnell, P.S.; Barrell, B.G.
Nature (1984) 310:207-21
DNA sequence and expression of the B95-8 Epstein-Barr virus
                                                                                                                                                                                                                                                                                                                                                                                                                     annotation; protein coding region
#superfamily herpesvirus 38K protein
#length 325 #molecular-weight 36462 #checksum 3547
                                                                          ##cross-references EMBL:V01555; NID:g59074; PID:g1334893
NCE A03794
##molecule_type DNA
##residues 1-325 ##label BAN
                                                                                                                                                                                                                                                                                                                                                                                          *cross-references MUID:84270667
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Score 64; DB 1; Length 325; Pred. No. 2.00e+01; 4; Mismatches 10; Indels 104 PELRDILQRILPPPNLEDSEALT 126 Ouery Match
Best Local Similarity 39.1%;
Matches 9; Conservative

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Gaps

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Search completed: Thu Jul 30 09:11:43 1998 Job time: 20 secs.

CARBOHYD CARBOHYD SEQUENCE Query Match

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셤 ð RESULT

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-!- IN CONTRAST TO YEAST CYCLASE, S.POWBE CYCLASE IS NOT LIKELY TO B REGULARIED BY RAS PROTEINS.
-!- SIMILARITY: THE REPEATED LEUCINE-RICH (LRR) SEGMENT IS FOUND IN MANY PROTEINS. NUMBER IN THIS PROTEIN: 22.
-!- SIMILARITY: DELONGS TO CLASS-3 OF ADENXIYL CYCLASES.
-!- SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
EMBL; M26492; G173339; --
PEREL; M34542; G173379; --
PIR; A33539; A33539.
YAMAWAKI-KATAOKA Y., TAMAOKI T., CHOE H.-R., TANAKA H., KATAOKA T
PROC. NYL., ACAD. SCI. U.S.A. 86:5693-6971(1989).
-!- FUNCTION: PLAYE SESENTIAL ROLES IN REGULATION OF CELLULAR
METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-2288C, AB972;
MEDLINE; 94378003.
JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER
                                                                                                                 -!- CATALYTIC ACTIVITY: ATP - 3',5'-CYCLIC AMP + PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1692;
                                                                                                                                                                                                                                                                                                                                                                   SYNTHESIS; MAGNESIUM
                                                                                                                                                                                                                                                                                                                                                                                       LEUCINE-RICH REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e 65; DB 1; Len
. No. 4.88e+00;
Mismatches 3;
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EURARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1993 (REL. 27, CREATED)
01-0CT-1993 (REL. 27, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
MRP4 OR YHLO04W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 AA.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                   CAMP
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MEDLINE: 92184810.
DAVIS S.C., TZAGOLOFF A., ELLIS S.
J. BIOL. CHEM. 267:5508-5514(1992)
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          888
888
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                                                                                                                                                                                                                                                                                                                                                                   LEUCINE-REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190333
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57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1692
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1692 AA;
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ID RTO4_YEAST
AC P32902;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN PAPILLOMAVIRUS TYPE 9.
VIRIDAE; DS-DNA NONENVELOPED VIRUSES; PAPOVAVIRIDAE; PAPILLOMAVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DELIGS H., TOFMANN B.;
CURR. TOP. MICROBIOL. IMMUNOL. 186:13-31(1994).
-!- FUNCTION: EZ IS A TRANSCRIPTIONAL TRANSCRIVATOR CAPABLE OF
ACTIVATIOR A CONDITIONAL ENHANCER IN THE VIRAL LONG CONTROL
REGION (LCR). EZ BINDS TO THE 5'-ACCGNNNCGGT-3' PALINDROMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P11299; 2BOP.
EARLY PROTEIN; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;
TRANS-ACTING FACTOR.
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                                                                                                                                                                                                      Score 67; DB 1; Length 1477; Pred. No. 2.34e+00;
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 66; DB 1; Length 461.
Pred. No. 3.39e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Mismatches 10; Indels
                                                                                                                                     POTENTIAL.
W; 79B302B8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EURARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52141 MW; DA2B4125 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
REGULATORY PROTEIN E2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1692 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   461 AA.
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                    POTENTIAL.
POTENTIAL.
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POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RSGPPGLOGRLORLLQASGNHAAGIL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBUNIT: BINDS DNA AS A DIMER.
EMBL; X74464; G397073; -.
PIR; S36593; S36593.
                                                                                                                                                            MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYAA_SCHPO STANDARD;
P14605;
01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQ
                                                  759
759
1345
1366
: 166727 M
                                                                                                                                                                                                                                                                                             499 GRLQSLLEAPEDDPNQMIEM 518
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GRLQRLLQASGNHAAGILTM 28
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38.5%;
                                                                                                                                                                                                        34.28;
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                                                                                                                                                                                                                                                    Conservative
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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MEDLINE; 90046723.
YOUNG D., RIGGS M.,
                                                                                                                                                                                                                        Best_Local Similarity
Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 94265501.
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SEQUENCE FROM N.A.
MEDLINE; 89345533.
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VE2_HPV09
P36780;
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SEQUENCE

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RESULT ID II AC P41 DT 01 DT 01 DF 01

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MEDLINE; 90130334.
MURPHY R.C., GASPARICH G.E., BRYANT D.A., PORTER R.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.1%;
Similarity 56.3%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 GPPGLPAHLDEELQAT 110
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73
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74
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PIR; A25720; LNHUP6.
PIR; B25720; LNHUP1.
HSSP: P02462; IBBE.
MIM; 178630; -.
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Matches 9; Conser
           92198680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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P19737;
SEQUENCE 1
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CONFLICT
CONFLICT
SEQUENCE
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DOMAIN
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CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
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VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSPA_HUMAN STANDARD; PRI; 248 AA.
97714,
01-APR-1998 (REL. 07, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
91 ONOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PULMONARY SURFACTANT ASSOCIATED PROFIEIN A PRECURSOR (SP-A) (PSP-A)
(PSAP) (ALVBOLAR PROTEINOSIS PROFIEIN)
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE; 97070356.

MORRIS J.C., FINNERTY H., BENNET F., TURNER K.J., WOOD C.R.;

EXP. HEMATOL. 24.1369-1376 (1996).

1- FUNCTION: THIS PROTEIN STIMULATES PLASMACYTOMA PROLIFERATION,

T-CELL-DEPENDENT DEVELOPMENT OF IMMUNOGLOBULIN-PRODUCING B

CELLS AND SYRERGIZES WITH IL-3 IN SUPPORTING MURINE

MEGARARYOCYTE COLONY FORMATION (BY SIMILARITY).

EMBL; U03421; G415654; --

MGD; MGI:107613; ILL1.

POTFENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2] SEQUENCE FROM N.A.
MEDLINE: 86014366.
WHITE R.T., DAMM D., MILLER J., SPRATT K., SCHILLING J., HAWGOOD BENSON B., CORDELL B.;
[3]
                                                                                                                                                                                                                                            EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 86250832.
FLOROS J., STEINBRINK R., JACOBS K., PHELPS D., KRIZ R.,
SULTZMAN L., JONES S., TAEUSCH H.W., FRANK H.A., FRITSCH
J. BIOL. CHEM. 261:9029-9033(1986).
                                    Length 879;
                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 63; DB 1; Len
Pred. No. 1.00e+01;
4; Mismatches 0;
 36 I -> L (IN REF. 3).
96834 MW; 8BFD7CF3 CRC32;
                                  Score 64; DB 1; L
Pred. No. 7.01e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                   21 POTENTIAL.
199 INTERLEUKIN-11.
21522 MW; 1CB30772 CRC32;
                                                                                                                                                                                       01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
INTERLEUKIN-11 PRECURSOR (IL-11).
                                                         5; Mismatches
                                                                                                                                                        199 AA
                                                                                                                                                        PRT:
                                                                                GVDGRLQAILQAHENELGDFVLHM 419
                                                                                               6 GLQGRLQRLLQASGNHAAG-ILTM 28
                                                                                                                                                                            (REL. 33, CREATED)
(REL. 33, LAST SEQ!
(REL. 35, LAST ANN
                                  32.7%;
ilarity 45.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 32.1%;
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFTPA OR SFTP1 OR PSAP
                                                                                                                                                                                                                                      MUS MUSCULUS (MOUSE).
                        128 ALQARLERLLR 138
36
879 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                        199 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 GLQGRLQRLLQ 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                          LT 12
IL11_MOUSE
P47873;
01-FEB-1996 (
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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HOMO

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MATTAL S.L., SINGH G., LOCKER J.L.;

AM. J. RESPIR. CELL MOL. BIOL. 6446-452(1992).

IL AM. J. RESPIR. CELL MOL. BIOL. 6446-452(1992).

PROSPHOLIPIDS AND CONTRIBUTES TO LOWER THE SUREACE TENSION AT THE PROSPHOLIPIDS AND CONTRIBUTES TO LOWER THE SUREACE TENSION AT THE ALVEOLI OF THE MAMMALIAN LUNG AND IS ESSENTIAL FOR NORMAL RESPIRATION.

I. SUBCELLULAR LOCATION: EXTRACELLULAR.

I. SUBCELLULAR LOCATION: EXTRACELLULAR.

I. SUBCELLULAR LOCATION: EXTRACELLULAR.

I. SUBCELLULAR SOCIATED PROTEIN: 2 COLLAGENOUS, CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-P) AND 2 SMALL HYDROPHOBIC CONTAINS (SP-C).

ENOTEIN (SP-B AND SP-C).

I. SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.

EMBL: M13666; G190670;

EMBL: M13666; G190672;

EMBL: M30838; G190672;

EMBL: M68519; G388049;

EMBL: M68519; G388049;

EMBL: M68519; G388049;

EMBL: M68519; G388049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSO0615; C_TYPE_LECTIN_1; 1.
PROSITE; PSO041; C_TYPE_LECTIN_2; 1.
GLYCOPROTETN; CALCIUM; SURFACE FILM; GASEOUS EXCHANGE; HYDROXYLATION;
SIGNAL; LECTIN; COLLAGEN; REPEAT; POLYMORPHISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PULMONARY SURFACTANT PROTEIN A.
COLLAGEN-LIKE (WITH HYDROXYPROLINE).
C-TYPE LECTIN (SHORT FORM).
BY SIMILARITY.
BY SIMILARITY.
PROBABLE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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4; Mismatches 3;
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R (IN G190565)
D (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P19737;
01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HYPOTHETICAL 28.7 KD PROTEIN IN RECA 3'REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Jul 30 09:12:01 1998; MasPar time 2.79 Seconds 251.630 Million cell updates/sec lar output not generated. Run on:

>US-08-938-548A-4 (1-28) from US08938548A.pep 196 1 RSGPPGLQGRLQASGNHAAGILIM 28 Description: Perfect Score: Title:

Sequence:

PAM 150 Gap 15 Scoring table:

Searched:

69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

swiss-prot35 1:swiss1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 31.467; Variance 48.238; scale 0.652

#### SUMMARIES

ult Vo. Score	:	% Query Match Length DB	82	£	Description	Pred. No.
7	1 36.2	2 398	Н	VE2_HPV63	REGULATORY PROTEIN E2.	5.14e-01
9	9 35.	2 736		ALD_MOUSE	ADRENOLEUKODYSTROPHY P	1.11e+00
φ	7 34.	2 79	-	NIFU_FRAAL	NIFU PROTEIN.	2.34e+00
ø	67 34.	2 442	-1	HRDB STRCO	RNA POLYMERASE PRINCIP	2.34e+00
9	67 34.	2 1477	Н	YOR1_YEAST	OLIGOMYCIN RESISTANCE	2.34e+00
9	6 33.7	7 461		VE2_HPV09	REGULATORY PROTEIN E2.	3.39e+00
9	65 33.	2 1692	ч	CYAA_SCHPO	ADENYLATE CYCLASE (EC	4.88e+00
Q	4 32.7	7 394	~1	RT04 YEAST	MITOCHONDRIAL 40S RIBO	7.01e+00
9	64 32.7	7 400	H	ASSY_SYNY3	ARGININOSUCCINATE SYNT	7.01e+00
φ	64 32.7	7 690		VTER EBV	PROBABLE DNA PACKAGING	7.01e+00
φ	64 32.7	7 879	Н	YDBH_ECOLI	HYPOTHETICAL 96.8 KD P	7.01e+00
Ö	9		-1	IL11_MOUSE	INTERLEUKIN-11 PRECURS	1.00e+01
φ	e e	1 248	ч	PSPA_HUMAN	PULMONARY SURFACTANT-A	1.00e+01
φ	9		Н	YREC_SYNP2	HYPOTHETICAL 28.7 KD P	1.00e+01
ဖ	3 32.1	1 324	Ч	ANX3_RAT	ANNEXIN III (LIPOCORTI	1.00e+01
v	3 32.1		Н	UL88_HCMVA	PROTEIN UL88.	1.00e+01
ø	3 32.	1 878	Н	ECR_DROME	ECDYSONE RECEPTOR (ECD	1.00e+01
φ	<u>س</u>	1 972	-	POLS_IPNVJ	STRUCTURAL POLYPROTEIN	1.00e+01
ဖ	3 32.1	Н	Н	PEX1_PICPA	PEROXISOME BIOSYNTHESI	1.00e+01
ဖ		_	ч	TR12_HUMAN	THYROID RECEPTOR INTER	1.00e+01
φ	62 31.6	6 187		MT28_YEAST	TRANSCRIPTIONAL ACTIVA	1.43e+01
ဖ	2 31.	6 511	Н	CTAQ_THEAQ	THERMOSTABLE CARBOXYPE	1.43e+01
ဖ	2 31.	6 624	-1	SIR_SYNP7	SULFITE REDUCTASE (FER	1.43e+01

1.43e+01	1.43e+01	1.43e+01	1.43e+01	1.43e+01	1.43e+01	2.02e+01	2.02e+01	2.02e+01	2.02e+01	2.02e+01	2.85e+01	2.85e+01	2.85e+01	2.85e+01	2.85e+01	2.85e+01	2.85e+01	2.85e+01	2.85e+01	2.85e+01	2.85e+01
GLYCOPROTEIN B PRECURS	STRUCTURAL POLYPROTEIN	NITRITE REDUCTASE (NAD	KINESIN-LIKE PROTEIN K	KINESIN-LIKE PROTEIN K	FATTY ACID SYNTHASE (E	NEGATIVE FACTOR (F-PRO	PULMONARY SURFACTANT-A	MATING-TYPE LOCUS ALLE	HYPOTHETICAL 57.9 KD P	SERINE/THREONINE PROTE	SPORE MATURATION PROTE	INTERLEUKIN-11 PRECURS	OROTIDINE 5'-PHOSPHATE	HYPOTHETICAL 34.8 KD P	OUTER MEMBRANE PROTEIN	FACTOR VIII INTRON 22	PROBABLE ATP SYNTHASE	ALANINE AMINOTRANSFERA	ALANINE AMINOTRANSFERA	RNA POLYMERASE SIGMA F	HC-TOXIN SYNTHETASE (E
VGLB_MCMVS	POLS_IPNVN	NIR_NEUCR	KF1A_HUMAN	KF1A_MOUSE	FAS_HUMAN	NEF_HV2NZ	PSPA_PIG	B7_USTMA	YB77_YEAST	AFSK_STRCO	SPMB_BACSU	IL11_HUMAN	DCOP_MYCBO	YP95_CAEEL	YOPM_YERPE	F812 MOUSE	HRB6_XANCV	ALAT_HUMAN	ALAT_RAT	RPSD_CAUCR	HIS1_COCCA
Н	-1	Н		Н	-	٦	7	7	Н	-	Н	Н	ч	ч	н	7	н	н	н	Н	н
928	972	1176	1690	1695	2504	180	249	410	520	799	179	199	274	302	367	380	442	495	495	652	5217
31.6	31.6	31.6	31.6	31.6	31.6	31.1	31.1	31.1	31.1	31.1	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6
62	62	62	62	62	62	61	61	61	61	61	9	9	09	9	09	09	9	9	09	9	9
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

1 pv63 standard: 398 aa.		1994		T-1994 (REL. 30, LAST ANNOTATION UPDATE)	REGULATORY PROTEIN E2.		HUMAN PAPILLOMAVIRUS TYPE 63.	VIRIDAE; DS-DNA NONENVELOPED VIRUSES; PAPOVAVIRIDAE; PAPILLOMAVIRUSES.		SEQUENCE FROM N.A.	MEDLINE; 93276568.	K., DELIUS H., MATSUKURA T., KAWASHIMA M., DE VILLIERS E.M.;	OGY 194:789-799(1993).	-1- FUNCTION: E2 IS A TRANSCRIPTIONAL TRANSACTIVATOR CAPABLE OF	CTIVATING A CONDITIONAL ENHANCER IN THE VIRAL LONG CONTROL	REGION (LCR). E2 BINDS TO THE 5'-ACCGNNNCGGT-3' PALINDROMIC	SEQUENCE.	-1- SUBUNIT: BINDS DNA AS A DIMER.	EMBL; X70828; G312096;	P11299; 2BOP.	EARLY PROTEIN; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;	TRANS-ACTING FACTOR; PHOSPHORYLATION.	NCE 398 AA; 45450 MW; C9BBOCEO CRC32;	(	Query Match Bost Local Similarity 55 6%: Dred No 5 14e-01:		
RESULT 1 TO VE2 HPV63	007850;	01-0CT-1994	01-0CT-1994	01-0CI-1994	REGULATORY	E2.	HUMAN PAPI	VIRIDAE; D	Ξ	SEQUENCE FI	MEDLINE; 93	EGAWA K., I	VIROLOGY 1	-1- FUNCTIO	ACTIVA	REGION	SEQUEN	-1- SUBUNI	EMBL; X708;	HSSP; P112	EARLY PROTI	TRANS-ACTI	SEQUENCE		Query Match Best Local Sir	Matches 10	
RESU	Ş	DŢ	ĮΩ	Ω	DE	GN	SO	8	RN	RP	æ	RA	RL	႘	ပ္ပ	႘	ပ္ပ	ပ္ပ	DR	DR	ΚW	ΚW	ÖS	•	no.	Ma	

295 RSPPKGGQSRLRRLIQEA 312 g

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736 AA. PRT; STANDARD; LT 2 ALD\_MOUSE P48410; RESULT

DALI

ACI

PALI

ACI

DT

O1

DT

O1

DE

ADI

OS

MU

CC

EU

RESULT

ALI

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01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
ADRENOLEUKODYSTROPHY PROTEIN HOMOLOG (ALDP).
ALD OR ALDGH.
MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
[1]

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N-PSDB; Q11010
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           complement components Gaa, Gaa and C5a; the inverse is found in albumin, vitamin D-binding protein and alpha-fetoprotein. The albumin, vitamin D-binding protein and alpha-fetoprotein. The disulphide-stabilized loop structure is thought to be conserved. The type II motif, related to repeats found in epidermal growth factor precursor is a 6-Cys pattern repeated nine times, although the ninth repeat in the A form is incomplete. Four of the repeats, (2, 3, 4 and 9) differ from the EGF-like motif in having a 4-6 residue insertion between cysteines 4 and 5 instead of the usual single residue. Embodied within repeats 5, 6, 7 and 8 is the consensus sequence for Asp and Ash hydroxylation. The 7th repeat contains the consensus O-glycosylation sequence, CXXXC.

Immediately following each repeat is a pentapeptide with the consensus sequence XD(IVY)(D/NBE. Fibulin binds to the cytopassing domain of the betal subunit of integrin adhesion receptors in a catton-dependent, EDTA-reversible manner. It can be used to manipulate adhesion of cells to fibronectin, collagen, laminin, and possibly also other proteins. Antibodies reactive with the protein have important diagnostic and therapeutic uses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
The same motif is found in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 601; 5.91e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beta-1 integrin; adhesion; receptor; fibronectin.
Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label - N-linked glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label - N-linked glycosylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   consensus pentapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label - consensus pentapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label = consensus pentapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glu/Asp-rich region
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/label= signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 96;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label type I motif
6..69
label repeat unit 1
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..311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 vplpllllgglallaagvdadvlleacc 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 VILLILILEPPALISIGYDAOPLPD-CC 39
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/label= fibulin C
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R11150 standard; Protein; 683 AA.
R11150;
21-MAY-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.1%;
Best Local Similarity 57.1%;
Matches 16; Conservative
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    R3
    R4
    R4
    R7
    R7

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Purified fibulin, DNA encoding it and antibodies reactive with it useful as diagnostic and therapeutic component.

Claim 10, Fig 5; 56pp; English.

The fibulin A, B and C forms are identical from their N-terminals to a divergence point at posn. 566 (terminal codon in fibulin A) at a which they are distinct, encoding polypeptides of 566, 601 and 683 residues resp. All three forms are rich in cysteine (11 %) and analysis with on and spacing of the Cys residues revealed two cys repeat lacking two Cys residues. The same motif is found in the repeat lacking two Cys residues. The same motif is found in complement components C3a, C4a and C5a; the inverse is found in albumin, vitamin D-binding protein and alpha-fetoprotein. The albumin, vitamin D-binding protein and alpha-fetoprotein. The calbumin, vitamin D-binding protein and alpha-fetoprotein. The factor precursor is a 6-Cys pattern repeated nine times, although the ninth repeat in the A form is incomplete. Four of the repeats of the A form is incomplete. Four of the usual single residue. Embodied within repeats 5, 6, 7 and 8 is the consensus sequence for Asp and Asn hydroxylation. The 7th repeat contains the consensus o-glycosylation sequence, CXCRPC.

Immediately following each repeat is a pentapeptide with the consensus sequence XD(I/V)(P/N)E. Fibulin binds to the cytoroplasmic domain of the betal subunit of integrin adhesion receptors in a cation-dependent, EDTA-reversible manner. It can be used to manipulate adhesion of cells to fibromectin, collagen, laminin, and possibly also other proteins. Antibodies reactive with the protein have importent diagnostic and therapeutic uses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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26-APR-1991 (first entry)
Natural recombinant human lecithin:cholesterol acyltransferase.
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consensus pentapeptide
                                                                                                                                                                                                                                                    consensus pentapeptide
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/label- consensus pentapeptide
                                                                                                                        'label consensus pentapeptide
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480..484
//label- re-
                                                                                                                                  403.439
/label= repeat unit 6
                                                          repeat unit 5
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ID P70134 standard; Protein; 440 AA.
AC P70134;
AZ 26-APR-1991 (first entry)
DE Natural recombinant human lecithiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-AUG-1990; U04662.
18-AUG-1989; US-395773.
(LJOL-) LA JOLLA CANCER RES.
(AMIN-) AMER NAT RED CROSS.
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/label= re
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WPI; 91-087250/12.
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Homo sapiens.
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R50009;
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Matches
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                                                                                                                                                                                                                                                                                                                              Pecombinant multimeric protein prodn. In bacteria - transfected with vector contg. new multi-cistronic expression unit, providing high level prodn. of pharmaceutical and cosmetic products Example 2.1.2; page 23-24; 42pp, German.
Plasmid pWW-2 contains the cDNA of the human PDGF-B gene, but with the 5'-translated region of the precursor being incomplete (see 080473, which encodes R6817). The BanHI/Noo! fragment of pWW-2 was used as the basis for mutagenesis to isolate the sequence coding for mature PDGF-B with a Met residue at the N-terminus. The mutagenised coding sequence was used in the construction of multicistronic expression units for recombinant expression of the PDGF-A/B dimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 4; 39pp; English.

Example 1 describes the subcloning and analysis of C-sis and V-sis genes encoding rPDGF B chain.

Clone U2-OS561 contains the c-sis gene encoding human PDGF B chain.

Exons 2-6 of this clone were subcloned and sequenced. They encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 1.94e+01;
11; Mismatches 6; Indels
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Pred. No. 1.94e+01;
11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           platelet-derived growth factor; wound healing; binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||||||::: |: :| :| | | ::|:|||: :||||
79 LQRLLQAN-GNH-AAGI-LTMGR-RAGAELEPYPCPGRR 113
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                                                                                                                                                  10-JUN-1993; 319708.
10-JUN-1993; DE-319708.
(BEIE) BEIERSDORF AG.
(GBEB) GBF GES BIOTECH FORSCHUNG GMBH.
ELCHNET W. MCCARTHY JEG, SCHNEPPE B; WPI; 95-022815/04.
N-PSDB; Q80473.
                                                                              /label- mature_PDGF-B
/label= pre-region
/note= "truncated"
57..216
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R40965 standard; Protein; 220 AA
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Best Local Similarity 43.6%;
Matches 17; Conservative
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Best Local Similarity 43.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thomason AR;
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10-MAR-1988; 302116.
13-MAR-1987; US-025344.
19-FEB-1988; US-152045.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 AA;
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EP-559234-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in bacteria.
                                                                                                        DE4319708-A
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                                                      protein
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PF 10
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79 LQRLLQAN-GNH-AAGI-LTMGR-RAGAELEPYPCPGRR 113

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N-PSDB; 058725.

New multicistronic expression units - for producing equimolar amis. of polypeptide(s) in mammalian cells as hosts

(Claim 11; Page 29; 109pp; German.

A PDGF-AB heterodimer is recombinantly produced using a bicistronic expression unit in which a sequence responsible for internal translation start is located between cistrons coding for the PDGF-B and PDGF-A chains. The preferred PDGF-B sequence for inclusion in the bliststronic construct is 058725 which codes for the precursor sequence 241 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New vectors expressing platelet-derived growth factor B epitope(s) - and contg. c-sis or v-sis genes portions; are used to promote wound healing and produce antibodies bisclosure; Fig 2: 49pp; English. Registed gescribes the amino acid sequence of recombinant platelet derived growth factor B c-sis (rPDGF B c-sis). It may be used to promote wound healing, or as an antigen to prepare antisera or sequence 241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUN-1995 (first entry)
Recombinant platelet derived growth factor B c-sis, Recombinant platelet derived growth factor B c-sis, rPDGF B c-sis; Synthetic.
                                                                                                                                                                                                                  /label= pre-peptide
82..190
/label= mature_PDGF-B
/note= "mature peptide is encoded by nucleotides
283-609 of Q58725"
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                                      29-5EP-1994 (first entry)
Platelet-derived Growth Factor PDGF-B precursor.
Platelet-Derived Growth Factor; heterodimer; PDGF-AB; recombliant protein production; PDGF-B chain; bicistronic vector system.
                                                                                                                                                                                                                                                                                                                                                                      26-AUG-1993; E02294.
27-AUG-1992; DB-228458.
(BEIE) BEIERSDORF AG.
(BERE) GBF GES BIOTECH FORSCHUNG GMBH.
Achterberg V, Dirks W, Dorschner A, Eichner W, E
Meyer-Ingold W, Mielke H, Wirth M, Doerschner A;
WPI: 94-101190/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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standard; Protein; 241 AA
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Nicolson MA, Thomason AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-NOV-1994.
10-MAR-1988; 302116.
13-MAR-1987; US-025344.
19-FEB-1988; US-152045.
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Disclosure; Fig 2; 78pp; English.

C vesicle and passaged a maximum of four times in cells in culture.

C vesicle and passaged a maximum of four times in cells in culture.

Viral DNA was prepd. from virons that accumulated in the cytoplasm of infected VERO cells (Kieff et al., J. Virol., 8, 125-132 (1971)).

C The Bamil SP junction fragments contg. the domain of the gene that specified ICP34.5 were cloned into a puC18 plasmid using HSV-1(F) sequences as probes in colony blot hybridisation. Further subclonings were done to facilitate sequencing of different regions of the gene. HSV may be rendered avizing HSV genome is useful for preparing a stable, non-transforming live viral vaccine which cells. The preparing a stable, non-transforming live viral vaccine which centured from a latent state.

See also R21706,7.

Sequence 252 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 RRPGPP-GLQGRLQRLLQANGNHAAGILTMGRRAGAELEPYPCPGRRCPTATATALAPRG 126
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Pred. No. 2.30e+01;
4; Mismatches 1; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Claim 23; page 42; 65pp; English.

The 4-1BB-L (ligand) protein is useful for exploring mechanisms of T-cell activation, as it is expressed on T lymphocytes. 4-1BB-L can be used as a tissue culture reagent for in vitro cultivation of primary T-cells during the derivation of clonal T-cell lines. It may also be used to stimulate proliferation of activated T-cells, used in therapeutic procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -cell; lymphocyte; activation; tissue culture; clone; cell lines;
roliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine.
deletion of ICP 34.5 gene encoding active gene prod.
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13; Mismatches 26; Indels
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R64190 standard; Protein; 254 AA.
R64190;
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07-MAY-1993; US-060843.
(IMMY) IMMUNEX CORP.
Alderson MR, Goodwin RG, 5
WPI; 95-022265/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.2%;
Best Local Similarity 34.4%;
atches 22; Conservative
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Best Local Similarity 66.7%;
Matches 12; Conservative
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127 GSRV 130
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